



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 116491

TO: Jeffrey Parkin
Location: REM-3D39/3C18
Art Unit: 1648
Monday, March 15, 2004
Case Serial Number: 10/055524

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: (571)272-2527

paul.schulwitz@uspto.gov

Search Notes

Examiner Parkin,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
STIC Biotech/Chem Library
(571)272-2527

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2004, 14:22:45 ; Search time 54 Seconds
(without alignments)
52.324 Million cell updates/sec

Title: PARKIN524.PEP
Perfect score: 46
Sequence: 1 kpvstcql11 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseq_29Jan04:*
2: geneseqp1980s:*
3: geneseqp1980s:*
4: geneseqp2000s:*
5: geneseqp2000s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004as:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	46	100.0	10	4	ABP16652
2	46	100.0	10	6	ABU69893
3	46	100.0	10	6	ABU70212
4	46	100.0	10	6	ABU70010
5	46	100.0	10	7	ADD96745
6	46	100.0	10	7	ADD96543
7	46	100.0	10	7	ADD96426
8	46	100.0	11	4	ABP17099
9	46	100.0	15	4	ABP24380
10	46	100.0	15	4	ABP24379
11	46	100.0	15	4	ABP24416
12	46	100.0	229	5	AAH48947
13	46	100.0	236	5	AAH51742
14	46	100.0	417	2	AAW43071
15	46	100.0	474	2	AAW37067
16	46	100.0	474	2	AAW37066
17	46	100.0	478	7	AAE39557
18	46	100.0	478	7	AAE39558
19	46	100.0	498	2	AAW37055
20	46	100.0	498	2	AAW37054
21	46	100.0	501	7	AAE39544
22	46	100.0	501	7	AAE39543
23	46	100.0	586	2	AAH49855
24	46	100.0	587	2	AAH49900
25	46	100.0	591	2	AAH49856

26	46	100.0	595	2	AAH29902	AAH29902 Human MCP
27	46	100.0	601	2	AAH29901	AAH29901 Human IP-
28	46	100.0	651	5	AAH4397	AAH4397 HIV ENV C
29	46	100.0	842	3	AAH69350	AAH69350 HIV-1 non
30	46	100.0	845	3	AAH69349	AAH69349 HIV-1 non
31	46	100.0	846	3	AAH69353	AAH69353 HIV-1 non
32	46	100.0	846	3	AAH69345	AAH69345 HIV-1 non
33	46	100.0	849	3	AAH69346	AAH69346 HIV-1 non
34	46	100.0	849	3	AAH69945	AAH69945 HIV synth
35	46	100.0	853	4	AAH82762	AAH82762 Ancestral
36	46	100.0	854	5	ABH06214	ABH06214 HIV Env 1
37	46	100.0	854	6	ABH06568	ABH06568 Human Imm
38	46	100.0	854	6	ABH05687	ABH05687 HIV Isola
39	46	100.0	854	7	ADC13221	ADC13221 Protein O
40	46	100.0	855	3	AAH69351	AAH69351 HIV-1 non
41	46	100.0	856	7	ABH80283	ABH80283 gp41 of 1
42	46	100.0	857	2	AAH12261	AAH12261 HIV-1 str
43	46	100.0	857	3	AAH69355	AAH69355 HIV-1 non
44	46	100.0	858	5	AAH48951	AAH48951 HIV-1 sub
45	46	100.0	859	1	AAH81865	AAH81865 Sequence

ALIGNMENTS

RESULT 1
ID ABP16652 standard; peptide; 10 AA.
XX
AC ABP16652;
XX
DT 11-SEP-2003 (revised)
DT 15-JUL-2002 (first entry)
XX
DE HIV B07 super motif env peptide #32.
XX
XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen;
KM vaccine; HIV infection; immunisation; virucide.
XX
OS Human immunodeficiency virus 1.
XX
PN WO200124810-A1.
XX
PD 12-APR-2001.
XX
PF 05-OCT-2000; 2000HO-US027766.
XX
PR 05-OCT-1999; 99US-00412863.
XX
PA (EPIM-) EPIMONE INC.
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Cells E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
PS Claim 32; Page 209; 448p; English.
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABU25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or

The invention describes a vaccine comprising a human immunodeficiency virus (HIV) vaccine candidate peptide containing an amino acid sequence selected from 669 amino acid sequences given in the specification, in an immunological excipient. The HIV vaccine peptides are useful as antigens for raising anti-HIV immune responses, such as T cell responses, and for inducing antibodies that react with HIV-1 and impairing viral multiplication *in vivo*. These antibodies reduce viral multiplication during any initial acute infection with HIV-1 and minimise chronic viraemia or progression leading to AIDS. This is the amino acid sequence

The invention describes a vaccine comprising a human immunodeficiency virus (HIV) vaccine candidate peptide containing an amino acid sequence selected from 669 amino acid sequences given in the specification, in an immunological adjuvant. The HIV vaccine peptides are useful as antigens for raising anti-HIV immune responses, such as T cell responses, and for inducing antibodies that react with HIV-1 and impairing viral multiplication *in vivo*. These antibodies reduce viral multiplication during an initial acute infection with HIV-1 and minimise chronic viraemia or progression leading to AIDS. This is the amino acid sequence of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide. (Updated on 23-OCT-2003 to standardise OS field).

Query Match	100.0%	Score 46;	DB 6;	Length 10;
Best Local Similarity	100.0%	Pred. No. 0.01;		
Matches 10;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

```

QY      1 KPVVSTQLLL 10
DB      1 KPVVSTQLLL 10

RESULT 4
ABU70010
ID      ABU70010 standard; peptide; 10 AA.
AC      ABU70010;
XX
XX
XX      23-OCT-2003 (revised)
DT      05-JUN-2003 (first entry)
XX
XX      Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #328.
DE
XX
XX      Human immunodeficiency virus; HIV; vaccine; immunological excipient;
KM      anti-HIV immune response; T cell response;
KM      viral multiplication inhibitor; chronic viraemia; AIDS.
XX
XX      Human immunodeficiency virus 1.
OS
XX      US2002182222-A1.
PN
XX
XX      05-DEC-2002.
PD
XX
XX      26-OCT-2001; 2001US-0005524.
PF
XX      10-JUL-1998; 98US-0092346P.
PR      08-JAN-1999; 99US-0115145P.
PR      23-APR-1999; 99US-0130677P.
PR      09-JUL-1999; 99US-00351036.
XX
XX      (GROO/) GROOT A D.
PA
XX
XX      Groot AD;
PI
XX
XX      WPI; 2003-352642/33.
DR
XX
XX      New vaccine comprising human immunodeficiency virus (HIV) vaccine
PT      candidate peptides, useful as antigens for raising anti-HIV immune
PT      responses, such as T cell responses, and for inducing antibodies and
PT      impairing viral multiplication.
XX
XX      Claim 1; Page 16; 32pp; English.
PS
XX
XX      The invention describes a vaccine comprising a human immunodeficiency
CC      virus (HIV) vaccine candidate peptide containing an amino acid sequence
CC      selected from 669 amino acid sequences given in the specification, in an
CC      immunological excipient. The HIV vaccine peptides are useful as antigens
CC      for raising anti-HIV immune responses, such as T cell responses, and for
CC      inducing antibodies that react with HIV-1 and impairing viral
CC      multiplication in vivo. These antibodies reduce viral multiplication
CC      during any initial acute infection with HIV-1 and minimise chronic
CC      viraemia or progression leading to AIDS. This is the amino acid sequence
CC      of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.
CC      (Updated on 23-OCT-2003 to standardise OS field)
XX
XX
SQ      Sequence 10 AA;

Query Match      100.0%; Score 46; DB 6; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVVSTQLLL 10
DB      1 KPVVSTQLLL 10

RESULT 5
ADD96745
ID      ADD96745 standard; peptide; 10 AA.
XX

```

```

AC      ADD96745;
XX
XX      29-JAN-2004 (first entry)
DT
XX
XX      HIV-1 cross-clade candidate peptide #530.
DE
XX
XX      HIV-1; cross-clade candidate peptide; HIV clade;
KM      major histocompatibility complex; MHC; human leukocyte antigen; HLA;
KM      T-cell activation; HIV positive patient; HIV infection; anti-HIV.
XX
XX      Human immunodeficiency virus 1.
OS
XX      US2003180314-A1.
PN
XX
XX      25-SEP-2003.
PD
XX
XX      22-JUL-2002; 2002US-00200708.
PF
XX      10-JUL-1998; 98US-0092346P.
PR      08-JAN-1999; 99US-0115145P.
PR      23-APR-1999; 99US-0130677P.
PR      09-JUL-1999; 99US-00351036.
XX
XX      (DEGR/) DEGROOT A.
PA
XX
XX      Degroot A;
PI
XX
XX      WPI; 2003-852210/79.
DR
XX
XX      New cross-clade HIV candidate peptide that binds a human major
PT      histocompatibility complex binding motif or activates T-cells from
PT      HIV positive patients, useful for preventing or treating HIV infection.
XX
XX      Example 3; SEQ ID NO 530; 146pp; English.
PS
XX
XX      The present invention relates to HIV-1 cross-clade candidate peptides
CC      comprising a sequence of about 8-50 amino acids, the sequence having
CC      complete, sequential sequence identity with a partial HIV-1 amino acid
CC      sequence that is absolutely conserved across at least 2 clades of HIV.
CC      The HIV-1 cross-clade candidate peptides possess at least one of the
CC      biological properties selected from (i) the ability to bind a human MHC
CC      histocompatibility complex (MHC) binding matrix motif for a human MHC
CC      allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the
CC      T2 in vitro peptide binding assay, and (iii) the ability to activate T-
CC      cells from HIV positive patients in at least one in vitro assay. The
CC      invention also discloses a pharmaceutical composition comprising the
CC      above peptide, and methods for the production and use of the cross-clade
CC      peptides. The composition and methods are useful in preventing or
CC      treating HIV infection. The present sequence represents a HIV-1 cross-
CC      clade candidate peptide.
XX
XX
SQ      Sequence 10 AA;

Query Match      100.0%; Score 46; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVVSTQLLL 10
DB      1 KPVVSTQLLL 10

RESULT 6
ADD96543
ID      ADD96543 standard; peptide; 10 AA.
AC      ADD96543;
XX
XX      29-JAN-2004 (first entry)
DT
XX
XX      HIV-1 cross-clade candidate peptide #328.
DE
XX
XX      HIV-1; cross-clade candidate peptide; HIV clade;

```


PA (EPTM-) EPTMONE INC.
 XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 DR
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 219; 448pp; English.
 XX
 CC The present invention describes a composition (1) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 46; DB 4; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVSTQALL 10
 DB 2 KPVSTQALL 11
 RESULT 9
 ABP24380
 ID ABP24380 standard; peptide; 15 AA.
 AC
 XX ABP24380;
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV DR super motif env peptide #2.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 PN WO200124810-A1.
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPTM-) EPTMONE INC.

PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;
 XX WPI; 2001-354887/37.
 DR
 XX
 PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 369; 448pp; English.
 XX
 CC The present invention describes a composition (1) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 CC
 SQ Sequence 15 AA;
 Query Match 100.0%; Score 46; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KPVSTQALL 10
 DB 2 KPVSTQALL 11
 RESULT 10
 ABP24379
 ID ABP24379 standard; peptide; 15 AA.
 AC
 XX ABP24379;
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV DR super motif env peptide #1.
 XX
 KW HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytototoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 PN WO200124810-A1.
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPTM-) EPTMONE INC.
 PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kubo RT, Grey HM;

PT peptide groups, useful for vaccinating against HIV-1.

CS Claim 32; Page 369; 448pp; English
XX

Sequence 15 AA:
The present invention describes a composition (I) comprising a prepared human immunodeficiency virus-1 (HIV-1) group comprising an amino acid sequence selected from 51 defined amino acid sequences (AB125347 to AB235397). (I) has virucide activity and can be used in vaccines. (I) may be used for immunising subjects against HIV-1 infections. The use of group-based vaccines has several advantages over traditional vaccines, particularly when compared to the use of whole antigens in vaccine compositions. There is evidence that the immune response to whole antigens is directed largely toward variable regions of the antigen, allowing for immune escape due to mutations. The groups for inclusion in an group-based vaccine may be selected from conserved regions of viral or tumour-associated antigens, which therefore reduces the likelihood of escape mutants. Furthermore, immunosuppressive groups that may be present in whole antigens can be avoided with the use of group-based vaccines. An additional advantage of an group-based vaccine approach is the ability to combine selected groups (CTL and HTLV), and further, to modify the composition of the groups, achieving, for example, enhanced immunogenicity. Accordingly, the immune response can be modulated, as appropriate, for the target disease. Similar engineering of the response is not possible with traditional approaches. AB11501 to AB23412 represent peptide sequences used in the exemplification of the present invention. (Updated on 11-Sep-2003 to standardise OS field)

XX Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
XX Claim 32; Page 369; 448pp; English.
XX
XX The present invention describes a composition (1) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (AB1253347 to
CC ABP25337). (1) has virucide activity and can be used in vaccines. (1) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. AB111501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
XX Sequence 15 AA;
SQ

```

SQ      Sequence 15 AA;
Query Match          100.0%; Score 46; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches    10; Conservative    0; Mismatches    0; Indels    0; Gaps    0.

QY      1 KPVVSTOLL 10
        |||||
db       1 KPVVSTOLL 10

```

Query Match	100.0%;	Score 46;	DB 4;	length 15;
Best Local Similarity	100.0%;	Pred. No. 0.016;		
Matches	10;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
QY	1	KPVVSTQILL	10	
Db	5	KPVVSTQILL	14	

```

RESULT 11
ABP24416
ID      ABP24416 standard; peptide; 15 AA
XX

```

AC ABP24416;
XY

DT	11-SEP-2003	(revised)
DT	15-JUL-2002	(first entry)
XX		

HIV DR super motif env peptide #38

vlf; tat; cytotoxic T lymphocyte; env; pol; gag; nef; vpr; vpu;
 vaccine; HIV infection; immunisation; virucide; antigen

Human immunodeficiency virus 1.

PN WO200124810-A1
YY

PD 12-APR-2001

05-OCT-2000; 2000MO-US027766

05-OCT-1999; 99US-00412863.

PA (EPIM-) EPIMUNE INC.
XX

WPI; 2001-354887/37.

	RESULT 12
ID	AAM48947
XX	AAM48947 standard; protein; 229 AA.
AC	AAM48947;
XX	
DT	29-AUG-2003 (revised)
DT	19-APR-2002 (first entry)
XX	
DE	HIV-1 subtype C env protein fragment consensus sequence.
XX	
KW	HIV-1 subtype C; vaccine; HIV infection; AIDS; env; antiviral.
XX	
OS	Human immunodeficiency virus; type I.
PN	WO20020494-A2.
XX	
PD	17-JAN-2002.
XX	
PF	09-JUL-2001; 2001MO-IB001208.
XX	
PR	07-JUL-2000; 2000US-021699SP.
PR	10-JUL-2000; 2000ZA-00003437.
XX	15-SEP-2000; 2000ZA-00004924.
PA	(MED-) MEDICAL RES COUNCIL.
PA	(UYCA-) UNIV CAPE TOWN.
PA	(UTNC-) UNIV NORTH CAROLINA.
ET	Williamson C, Swanstrom RI, Morris L, Karim SA, Johnston RE
XX	WPI; 2002-171700/22.

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2004, 14:22:50 ; Search time 23 Seconds
(without alignments)
22.446 Million cell updates/sec

Title: PARKIN524.PEP
Perfect score: 46
Sequence: 1 kpvstqlll 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/2/1aa/5A_COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B_COMB.pep:*
3: /cgn2_6/prodata/2/1aa/6A_COMB.pep:*
4: /cgn2_6/prodata/2/1aa/6B_COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfillseq.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	474	3	US-08-889-841B-36 Sequence 36, Appl
2	46	100.0	474	3	US-08-889-841B-39 Sequence 39, Appl
3	46	100.0	474	4	US-09-419-362-36 Sequence 36, Appl
4	46	100.0	474	4	US-09-419-362-39 Sequence 39, Appl
5	46	100.0	498	3	US-08-889-841B-2 Sequence 2, Appl
6	46	100.0	498	3	US-08-889-841B-5 Sequence 5, Appl
7	46	100.0	498	4	US-09-419-362-2 Sequence 2, Appl
8	46	100.0	498	4	US-09-419-362-5 Sequence 5, Appl
9	46	100.0	587	4	US-09-646-028-50 Sequence 50, Appl
10	46	100.0	595	4	US-09-646-028-56 Sequence 56, Appl
11	46	100.0	596	2	US-08-392-806A-2 Sequence 2, Appl
12	46	100.0	596	2	US-09-257-490-2 Sequence 2, Appl
13	46	100.0	600	3	US-08-392-806A-4 Sequence 4, Appl
14	46	100.0	600	3	US-09-257-490-4 Sequence 4, Appl
15	46	100.0	601	4	US-09-646-028-52 Sequence 52, Appl
16	46	100.0	613	3	US-09-257-490-11 Sequence 11, Appl
17	46	100.0	855	4	US-09-206-551-11 Sequence 11, Appl
18	46	100.0	855	4	US-09-206-551-12 Sequence 12, Appl
19	43	93.5	15	4	US-09-009-953-269 Sequence 269, Appl
20	43	93.5	20	1	US-08-218-025A-52 Sequence 52, Appl
21	43	93.5	21	1	US-08-218-025A-147 Sequence 147, Appl
22	43	93.5	21	3	US-09-220-389A-1 Sequence 1, Appl
23	43	93.5	22	1	US-08-218-025A-110 Sequence 110, Appl
24	43	93.5	22	1	US-08-218-025A-143 Sequence 143, Appl
25	43	93.5	22	2	US-08-493-235-19 Sequence 19, Appl
26	43	93.5	84	4	US-09-536-977-10 Sequence 10, Appl
27	43	93.5	425	4	US-09-536-977-46 Sequence 46, Appl

28	43	93.5	425	4	US-09-536-977-48 Sequence 48, Appl
29	43	93.5	425	4	US-09-536-977-50 Sequence 50, Appl
30	43	93.5	425	4	US-09-536-977-52 Sequence 52, Appl
31	43	93.5	455	3	US-08-889-841B-46 Sequence 46, Appl
32	43	93.5	455	4	US-09-419-362-46 Sequence 46, Appl
33	43	93.5	469	3	US-08-889-841B-23 Sequence 23, Appl
34	43	93.5	469	4	US-09-419-362-23 Sequence 23, Appl
35	43	93.5	476	4	US-09-536-977-74 Sequence 74, Appl
36	43	93.5	479	2	US-08-037-816A-20 Sequence 20, Appl
37	43	93.5	479	2	US-08-037-816A-24 Sequence 24, Appl
38	43	93.5	479	2	US-08-530-146-20 Sequence 20, Appl
39	43	93.5	479	2	US-08-530-146-24 Sequence 24, Appl
40	43	93.5	479	5	PCT-US91-02166-10 Sequence 10, Appl
41	43	93.5	479	5	PCT-US91-02250-1 Sequence 1, Appl
42	43	93.5	483	3	US-08-889-841B-31 Sequence 31, Appl
43	43	93.5	484	4	US-09-419-362-31 Sequence 31, Appl
44	43	93.5	484	2	US-08-037-816A-22 Sequence 22, Appl
45	43	93.5	484	2	US-08-530-146-22 Sequence 22, Appl

ALIGNMENTS

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RESULT 1
US-08-889-841B-36
; Sequence 36, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; PRIOR FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 36
; LENGTH: 474
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-36

Query Match      100.0%; Score 46; DB 3; Length 474;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSTQLLL 10
Db      207 KPVSTQLLL 216

RESULT 2
US-08-889-841B-39
; Sequence 39, Application US/08889841B
; GENERAL INFORMATION:
; APPLICANT: Berman, Phillip W.
; TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
; FILE REFERENCE: 14918-703CIP
; CURRENT APPLICATION NUMBER: US/08/889,841B
; CURRENT FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: US 60/676,737
; PRIOR FILING DATE: 1996-07-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 474
; TYPE: PRT
; ORGANISM: HIV
US-08-889-841B-39

Query Match      100.0%; Score 46; DB 3; Length 474;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 KPVVSTOLL 10
Db 207 KPVVSTOLL 216

RESULT 3

US-09-419-362-36
Sequence 36, Application US/09419362
Patent No. 6585979
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703DIV1
CURRENT APPLICATION NUMBER: US/09/419,362
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: US 08/889,841
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 36
LENGTH: 474
TYPE: PRT
ORGANISM: HIV
US-09-419-362-36

Query Match
Best Local Similarity 100.0%; Score 46; DB 4; Length 474;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVVSTOLL 10
Db 207 KPVVSTOLL 216

RESULT 4

US-09-419-362-39
Sequence 39, Application US/09419362
Patent No. 6585979
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703DIV1
CURRENT APPLICATION NUMBER: US/09/419,362
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: US 08/889,841
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 474
TYPE: PRT
ORGANISM: HIV
US-09-419-362-39

Query Match
Best Local Similarity 100.0%; Score 46; DB 4; Length 474;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVVSTOLL 10
Db 207 KPVVSTOLL 216

RESULT 5

US-08-889-841B-2
Sequence 2, Application US/0889841B
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.

TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 498
TYPE: PRT
ORGANISM: HIV
US-08-889-841B-2

Query Match
Best Local Similarity 100.0%; Score 46; DB 3; Length 498;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVVSTOLL 10
Db 232 KPVVSTOLL 241

RESULT 6

US-08-889-841B-5
Sequence 5, Application US/0889841B
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703CIP
CURRENT APPLICATION NUMBER: US/08/889,841B
CURRENT FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 498
TYPE: PRT
ORGANISM: HIV
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(498)
OTHER INFORMATION: Xaa = Any Amino Acid
US-08-889-841B-5

Query Match
Best Local Similarity 100.0%; Score 46; DB 3; Length 498;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVVSTOLL 10
Db 232 KPVVSTOLL 241

RESULT 7

US-09-419-362-2
Sequence 2, Application US/09419362
Patent No. 6585979
GENERAL INFORMATION:
APPLICANT: Berman, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703DIV1
CURRENT APPLICATION NUMBER: US/09/419,362
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: US 08/889,841
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 2
LENGTH: 498

TYPE: PRT
ORGANISM: HIV
US-09-419-362-2

Query Match
Best Local Similarity 100.0%; Score 46; DB 4; Length 498;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTOLL 10
DB 232 KPVSSTOLL 241

RESULT 8
US-09-419-362-5
Sequence 5, Application US/09419362
Patent No. 6585979

GENERAL INFORMATION:
APPLICANT: Bertram, Phillip W.
TITLE OF INVENTION: HIV ENVELOPE POLYPEPTIDES AND VACCINE
FILE REFERENCE: 14918-703DIV1
CURRENT APPLICATION NUMBER: US/09/419,362
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: US 08/889,841
PRIOR FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: US 60/676,737
PRIOR FILING DATE: 1996-07-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 498
TYPE: PRT
ORGANISM: HIV
FEATURE:
NAME/KEY: VARIANT
LOCATION: (1)...(498)
OTHER INFORMATION: Xaa = Any Amino Acid
US-09-419-362-5

Query Match
Best Local Similarity 100.0%; Score 46; DB 4; Length 498;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTOLL 10
DB 232 KPVSSTOLL 241

RESULT 9
US-09-646-028-50
Sequence 50, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014,0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 587
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-50

Query Match 100.0%; Score 46; DB 4; Length 587;

Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTOLL 10
DB 328 KPVSSTOLL 337

RESULT 10
US-09-646-028-56
Sequence 56, Application US/09646028
Patent No. 6562347
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014,0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 56
LENGTH: 595
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-56

Query Match
Best Local Similarity 100.0%; Score 46; DB 4; Length 595;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTOLL 10
DB 336 KPVSSTOLL 345

RESULT 11
US-08-392-806A-2
Sequence 2, Application US/08392806A
Patent No. 5965135
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: New HIV-1 virus isolates of a
TITLE OF INVENTION: subtype, vaccine against HIV-1 virus infections of this subtype
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jacobson, Price Holman and Stern, PLLC
STREET: 400 Seventh street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,806A
FILING DATE: 20-APR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/02275
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4228787.1
FILING DATE: 29-AUG-1992

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 596 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-392-806A-2

Query Match
Best Local Similarity 100.0%; Score 46; DB 2; Length 596;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
Db 137 KPVSSTQLL 146

RESULT 12
US-09-257-490-2

Sequence 2, Application US/09257490A
Patent No. 6248328

GENERAL INFORMATION:

APPLICANT: Dietrich, Ursula

APPLICANT: Von Briesen, Hagen

APPLICANT: Grez, Manuel

APPLICANT: Rubsamen-Waigmann, Helga

TITLE OF INVENTION: HIV-1 virus isolates of a subtype and its differential

TITLE OF INVENTION: diagnostic, a vaccine against HIV-1 virus infections

TITLE OF INVENTION: of this subtype and method of producing same, use of

FILE REFERENCE: 10496/P585120S1

CURRENT APPLICATION NUMBER: US/09/257,490A

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 2

LENGTH: 596

TYPE: PRT

ORGANISM: Human immunodeficiency virus

FEATURE:

OTHER INFORMATION: HIV-1(D757)

Query Match
Best Local Similarity 100.0%; Score 46; DB 3; Length 596;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
Db 137 KPVSSTQLL 146

RESULT 13

US-08-392-806A-4

Sequence 4, Application US/08392806A
Patent No. 5865135

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: New HIV-1 virus isolates of a

TITLE OF INVENTION: subtype, vaccine against HIV-1 virus infections of this subtype

TITLE OF INVENTION: and method of producing same, use of the HIV-1 virus isolates

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Jacobson, Price Holman and Stern, PLLC

STREET: 400 Seventh street, N.W.

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/392,806A
FILING DATE: 20-APR-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/02275
FILING DATE: 25-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P4228787.1
FILING DATE: 29-AUG-1992
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 600 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-392-806A-4

Query Match
Best Local Similarity 100.0%; Score 46; DB 2; Length 600;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
Db 139 KPVSSTQLL 148

RESULT 14

US-09-257-490-4

Sequence 4, Application US/09257490A
Patent No. 6248328

GENERAL INFORMATION:

APPLICANT: Dietrich, Ursula

APPLICANT: Von Briesen, Hagen

APPLICANT: Grez, Manuel

APPLICANT: Rubsamen-Waigmann, Helga

TITLE OF INVENTION: HIV-1 virus isolates of a subtype and its differential

TITLE OF INVENTION: diagnostic, a vaccine against HIV-1 virus infections

TITLE OF INVENTION: of this subtype and method of producing same, use of

FILE REFERENCE: 10496/P585120S1

CURRENT APPLICATION NUMBER: US/09/257,490A

NUMBER OF SEQ ID NOS: 15

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 600

TYPE: PRT

ORGANISM: Human immunodeficiency virus

FEATURE:

OTHER INFORMATION: HIV-1(D747)

US-09-257-490-4

Query Match
Best Local Similarity 100.0%; Score 46; DB 3; Length 600;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
Db 139 KPVSSTQLL 148

RESULT 15

US-09-646-028-52

Sequence 52, Application US/09646028
Patent No. 6562347

GENERAL INFORMATION:

APPLICANT: Kwak, Larry

APPLICANT: Biragyn, Atya

TITLE OF INVENTION: METHODS AND COMPOSITIONS OF

TITLE OF INVENTION: CHECKKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES

FILE REFERENCE: 14014.0316/P

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; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-52

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Query Match      100.0%; Score 46; DB 4; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 KPVSTQLL 10
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Db      342 KPVSTQLL 351

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OM protein - protein search, using sw model

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Title: PARKIN24.PEP
Perfect score: 46
Sequence: 1 kpvstqlll 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Published Applications_AA.*
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8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10C_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	10	US-10-200-708-211	Sequence 211, App
2	46	100.0	10	US-10-200-708-328	Sequence 328, App
3	46	100.0	10	US-10-200-708-530	Sequence 530, App
4	46	100.0	236	US-09-827-688-2	Sequence 2, Appl
5	46	100.0	587	US-10-335-394-50	Sequence 50, Appl
6	46	100.0	585	US-10-335-394-56	Sequence 56, Appl
7	46	100.0	601	US-10-335-394-52	Sequence 52, Appl
8	46	100.0	803	US-10-190-435-134	Sequence 134, App
9	46	100.0	803	US-10-190-435-135	Sequence 135, App
10	46	100.0	845	US-10-190-435-129	Sequence 129, App
11	46	100.0	845	US-10-190-435-130	Sequence 130, App
12	46	100.0	845	US-10-190-435-143	Sequence 143, App
13	46	100.0	849	US-10-190-435-148	Sequence 148, App
14	46	100.0	851	US-10-190-435-131	Sequence 131, App
15	46	100.0	851	US-10-190-435-149	Sequence 149, App

16	46	100.0	853	14	US-10-190-435-133	Sequence 133, App
17	46	100.0	854	14	US-10-190-435-5	Sequence 5, Appl
18	46	100.0	854	14	US-10-190-435-128	Sequence 128, App
19	46	100.0	854	14	US-10-241-009-5	Sequence 5, Appl
20	46	100.0	854	14	US-10-190-434B-5	Sequence 5, Appl
21	46	100.0	854	14	US-10-190-305A-5	Sequence 5, Appl
22	46	100.0	855	14	US-10-190-435-144	Sequence 144, App
23	46	100.0	855	14	US-10-369-294-11	Sequence 11, App
24	46	100.0	855	14	US-10-369-294-12	Sequence 12, App
25	46	100.0	857	14	US-10-190-435-132	Sequence 132, App
26	46	100.0	857	14	US-10-190-435-138	Sequence 138, App
27	46	100.0	858	14	US-10-190-435-150	Sequence 150, App
28	46	100.0	859	14	US-10-190-435-137	Sequence 137, App
29	46	100.0	860	14	US-10-190-435-6	Sequence 6, Appl
30	46	100.0	860	14	US-10-190-435-145	Sequence 145, App
31	46	100.0	860	14	US-10-190-435-146	Sequence 146, App
32	46	100.0	860	14	US-10-241-009-6	Sequence 6, Appl
33	46	100.0	860	14	US-10-190-434B-6	Sequence 6, Appl
34	46	100.0	860	14	US-10-190-305A-6	Sequence 6, Appl
35	46	100.0	861	14	US-10-190-435-139	Sequence 139, App
36	46	100.0	862	14	US-10-190-435-141	Sequence 141, App
37	46	100.0	862	14	US-10-190-435-142	Sequence 142, App
38	46	100.0	865	14	US-10-190-435-140	Sequence 140, App
39	46	100.0	867	14	US-10-190-435-3	Sequence 3, Appl
40	46	100.0	867	14	US-10-190-435-126	Sequence 126, App
41	46	100.0	867	14	US-10-241-009-3	Sequence 3, Appl
42	46	100.0	867	14	US-10-190-434B-3	Sequence 3, Appl
43	46	100.0	867	14	US-10-190-305A-3	Sequence 3, Appl
44	46	100.0	869	14	US-10-190-435-4	Sequence 4, Appl
45	46	100.0	869	14	US-10-241-009-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-10-200-708-211
; Sequence 211, Application US/10200708
; Publication No. US20030180314A1
; GENERAL INFORMATION:
; APPLICANT: Degroot, Anne S.
; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
; FILE REFERENCE: 17999-001
; CURRENT APPLICATION NUMBER: US/10/200,708
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US/09/351,036
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,346
; PRIOR FILING DATE: 1998-07-10
; PRIOR APPLICATION NUMBER: 60/115,145
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: 60/130,677
; PRIOR FILING DATE: 1999-04-23
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 211
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus
US-10-200-708-211
Query Match 100.0%; Score 46; DB 14; Length 10;
Best Local Similarity 100.0%; Pred No. 0.01; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVSQTLL 10
Db 1 KPVSQTLL 10
RESULT 2
US-10-200-708-328
; Sequence 328, Application US/10200708

```
Publication No. US20030180314A1
GENERAL INFORMATION:
APPLICANT: Degroot, Anne S.
TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
FILE REFERENCE: 1799-001
CURRENT APPLICATION NUMBER: US/10/200,708
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/351,036
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 60/092,346
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/115,145
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 60/130,677
PRIOR FILING DATE: 1999-04-23
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 328
LENGTH: 10
TYPE: PRT
ORGANISM: Human Immunodeficiency virus
US-10-200-708-328
```

```
Query Match
Best Local Similarity 100.0%; Score 46; DB 14; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTOLL 10
Db 1 KPVVSTOLL 10
```

```
RESULT 3
US-10-200-708-530
Sequence 530, Application US/10200708
Publication No. US20030180314A1
GENERAL INFORMATION:
APPLICANT: Degroot, Anne S.
TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
FILE REFERENCE: 1799-001
CURRENT APPLICATION NUMBER: US/10/200,708
CURRENT FILING DATE: 2002-07-22
PRIOR APPLICATION NUMBER: US/09/351,036
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: 60/092,346
PRIOR FILING DATE: 1998-07-10
PRIOR APPLICATION NUMBER: 60/115,145
PRIOR FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 60/130,677
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 530
LENGTH: 10
TYPE: PRT
ORGANISM: Human Immunodeficiency virus
US-10-200-708-530
```

```
Query Match
Best Local Similarity 100.0%; Score 46; DB 14; Length 10;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTOLL 10
Db 1 KPVVSTOLL 10

RESULT 4
US-09-827-688-2
Sequence 2, Application US/09827688
Publication No. US20030165476A1
GENERAL INFORMATION:
APPLICANT: ORSON, FRANK
```

```
APPLICANT: KINSEY, BERNA
APPLICANT: BHOGAL, BALBIR
TITLE OF INVENTION: MACROAGGREGATED PROTEIN CONJUGATES AS ORAL GENETIC IMMUNIZATION DI
FILE REFERENCE: P01949US/110004014
CURRENT APPLICATION NUMBER: US/09/827,688
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: 60/195,680
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn version 3.0
SEQ ID NO 2
LENGTH: 236
TYPE: PRT
ORGANISM: HIV U#23
US-09-827-688-2
```

```
Query Match
Best Local Similarity 100.0%; Score 46; DB 10; Length 236;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTOLL 10
Db 46 KPVVSTOLL 55
```

```
RESULT 5
US-10-335-394-50
Sequence 50, Application US/10335394
Publication No. US20030138452A1
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/10/335,394
CURRENT FILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US/09/646,028
PRIOR FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 587
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of artificial sequence; note=synthetic construct
US-10-335-394-50
```

```
Query Match
Best Local Similarity 100.0%; Score 46; DB 14; Length 587;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTOLL 10
Db 328 KPVVSTOLL 337
```

```
RESULT 6
US-10-335-394-56
Sequence 56, Application US/10335394
Publication No. US20030138452A1
GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biregyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/10/335,394
CURRENT FILING DATE: 2002-12-31
```

```

; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 56
; LENGTH: 595
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-56

Query Match      100.0%; Score 46; DB 14; Length 595;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSTQLL 10
Db      336 KPVSTQLL 345

RESULT 7
US-10-335-394-52
; Sequence 52, Application US/10335394
; Publication No. US20030138452A1
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Biragyn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/10/335,394
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US/09/646,028
; PRIOR FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 601
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-10-335-394-52

Query Match      100.0%; Score 46; DB 14; Length 601;
Best Local Similarity 100.0%; Pred. No. 0.86;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSTQLL 10
Db      342 KPVSTQLL 351

RESULT 8
US-10-190-435-134
; Sequence 134, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: P18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
```

```

; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 134
; LENGTH: 803
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TV007CB104
US-10-190-435-134

Query Match      100.0%; Score 46; DB 14; Length 803;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSTQLL 10
Db      252 KPVSTQLL 261

RESULT 9
US-10-190-435-135
; Sequence 135, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: P18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 135
; LENGTH: 803
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: TV007CB105
US-10-190-435-135

Query Match      100.0%; Score 46; DB 14; Length 803;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KPVSTQLL 10
Db      252 KPVSTQLL 261

RESULT 10
US-10-190-435-129
; Sequence 129, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: P18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 129
; LENGTH: 845
; TYPE: PRF
```

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TV012c2.1
US-10-190-435-129

Query Match
Best Local Similarity 100.0%; Score 46; DB 14; Length 845;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
DB 242 KPVSSTQLL 251

RESULT 11
US-10-190-435-130
Sequence 130, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: VAN RENSBERG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
FILE REFERENCE: P18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 130
LENGTH: 845
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TV012c2.2
US-10-190-435-130

Query Match
Best Local Similarity 100.0%; Score 46; DB 14; Length 845;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
DB 242 KPVSSTQLL 251

RESULT 12
US-10-190-435-143
Sequence 143, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: VAN RENSBERG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
FILE REFERENCE: P18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 143
LENGTH: 845
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TV003ce260
US-10-190-435-143

Query Match
Best Local Similarity 100.0%; Score 46; DB 14; Length 845;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
DB 240 KPVSSTQLL 249

RESULT 13
US-10-190-435-148
Sequence 148, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: VAN RENSBERG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
FILE REFERENCE: P18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 148
LENGTH: 849
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: 96BWS.02
US-10-190-435-148

Query Match
Best Local Similarity 100.0%; Score 46; DB 14; Length 849;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
DB 250 KPVSSTQLL 259

RESULT 14
US-10-190-435-131
Sequence 131, Application US/10190435
Publication No. US20030143248A1
GENERAL INFORMATION:
APPLICANT: ZUR MEGEDE, Jan
APPLICANT: BARNETT, Susan W.
APPLICANT: LIAN, Ying
APPLICANT: ENGELBRECHT, Susan
APPLICANT: VAN RENSBERG, Estrelita J.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
FILE REFERENCE: P18133.003 / 2302-18133
CURRENT APPLICATION NUMBER: US/10/190,435
CURRENT FILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 319
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 131
LENGTH: 851
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: TV006c9.1
US-10-190-435-131

Query Match
Best Local Similarity 100.0%; Score 46; DB 14; Length 851;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10

Db 247 KPVSSTOLL 256

RESULT 15
US-10-190-435-149

; Sequence 149, Application US/10190435
; Publication No. US20030143248A1
; GENERAL INFORMATION:
; APPLICANT: ZUR MEGEDE, Jan
; APPLICANT: BARNETT, Susan W.
; APPLICANT: LIAN, Ying
; APPLICANT: ENGELBRECHT, Susan
; APPLICANT: VAN RENSBURG, Estrelita J.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING ANTIGENIC HIV TYPE C
; TITLE OF INVENTION: POLYPEPTIDES, POLYPEPTIDES AND USES THEREOF
; FILE REFERENCE: P18133.003 / 2302-18133
; CURRENT APPLICATION NUMBER: US/10/190,435
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 149
; LENGTH: 851
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: ETH2220
US-10-190-435-149

Query Match 100.0%; Score 46; DB 14; Length 851;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTOLL 10
Db 249 KPVSSTOLL 258

Search completed: March 12, 2004, 14:30:42
Job time : 34 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2004, 14:22:50 ; Search time 21 Seconds
(without alignments)
45.805 Million cell updates/sec

Title: PARKIN524.PEP
Perfect score: 46
Sequence: 1 kpvstqlll 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	495	2	S11493 env polypeptide -
2	46	100.0	859	2	T01672 envelope polypeptide
3	43	93.5	219	2	S25939 env protein - huma
4	43	93.5	729	1	VCLJXK env polypeptide pr
5	43	93.5	843	1	H44001 env polypeptide pr
6	43	93.5	846	1	VCLJND env polypeptide pr
7	43	93.5	847	2	T09448 envelope glycoprote
8	43	93.5	847	2	S13289 env protein - huma
9	43	93.5	851	2	S13985 env polypeptide -
10	43	93.5	852	1	VCLJBR env polypeptide -
11	43	93.5	852	2	T12016 envelope glycoprote
12	43	93.5	853	2	S54384 envelope polypept
13	43	93.5	854	2	S13288 env protein huma
14	43	93.5	855	1	VCLJZR env polypeptide pr
15	43	93.5	856	1	VCLJH3 env polypeptide pr
16	43	93.5	856	1	VCLJVL env polypeptide pr
17	43	93.5	856	1	VCLJ3W env polypeptide pr
18	43	93.5	856	1	A44963 env polypeptide pr
19	43	93.5	859	1	VCLJMN env polypeptide pr
20	43	93.5	861	1	VCLJLV env polypeptide pr
21	43	93.5	861	1	VCLJKB env polypeptide pr
22	43	93.5	868	1	VCLJH4 env polypeptide -
23	42	91.3	506	2	A40218 envelope glycoprote
24	42	91.3	855	1	VCLJAZ env polypeptide pr
25	41	89.1	854	1	VCLJSI env polypeptide pr
26	40	87.0	877	2	S49197 envelope protein p
27	38	82.6	861	1	VCLJSC env polypeptide p
28	37	80.4	863	2	A53034 gag polypeptide -
29	34	73.9	224	2	S71749 DCL protein precu

30	34	73.9	443	2	C41621 env polypeptide p
31	34	73.9	445	2	A41621 env polypeptide M
32	34	73.9	454	2	B41621 env polypeptide D
33	34	73.9	486	2	S06949 achaeete-secute locu
34	33	71.7	540	2	T51390 TCP-1 chaperonin-1
35	33	71.7	876	2	AB1177 cation transportin
36	33	71.7	876	2	AF1534 cation transportin
37	32	69.6	130	2	T51684 probable transcrip
38	32	69.6	213	2	F84532 hypothetical prote
39	32	69.6	254	2	C70387 dehydrogenase - Ag
40	32	69.6	255	2	S50326 phosphoglycerate m
41	32	69.6	369	2	I64234 competence locus B
42	32	69.6	454	2	S61019 hypothetical prote
43	32	69.6	638	2	T22518 hypothetical prote
44	32	69.6	662	2	G82721 regulator of patho
45	32	69.6	868	2	B82213 aconitate hydratase

ALIGNMENTS

RESULT 1
S31493
env polypeptide - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 26-Aug-1999
C:Accession: S31493
R:Clagg, C.S.
Submitted to the EMBL Data Library, December 1992
A:Reference number: S31493
A:Accession: S31493
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-495 <CLF>
A:Cross-references: EMBL:Z19533; NID:G60244; PIDN:CAA79593.1; PID:G60245
C:Superfamily: type B retrovirus env polypeptide
C:Keywords: polypeptide

Query Match 100.0%; Score 46; DB 2; Length 495;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLLL 10
DB 233 KPVSSTQLLL 242

RESULT 2

T01672
envelope polypeptide precursor - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 21-Jul-2000
C:Accession: T01672
R:Alizon, M.; Main-Hobson, S.; Gluckman, J.C.; Sonigo, P.
Cell 46, 63-74, 1986
A:Title: Genetic variability of the AIDS virus: Nucleotide sequence analysis of two isol:
A:Reference number: Z14389; NUID:86245056; PMID:2424612
A:Accession: T01672
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-859 <ALI>
A:Cross-references: EMBL:K03456; NID:G60228; PIDN:CAA28016.1; PID:G60234
C:Superfamily: type B retrovirus env polypeptide

Query Match 100.0%; Score 46; DB 2; Length 859;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLLL 10
DB 257 KPVSSTQLLL 266

RESULT 3

S25939
env protein - human immunodeficiency virus type 1 (fragment)
C:Species: human immunodeficiency virus type 1, HIV-1
C>Date: 25-Feb-1994 #sequence_revision 30-Jan-1998 #text_change 26-Aug-1999
C:Accession: S25939
R:Quo, H.G.; Chermann, J.C.; Waters, D.; Hall, L.; Louie, A.; Gallo, R.C.; Streicher, H.
Nucleotide: 745-746, 1991
A:Title: Sequence analysis of original HIV-1
A:Reference number: S25937; MUID:91156044; PMID:2000145
A:Accession: S25939
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-219 <GDU>
A:Cross-references: EMBL:X57447; NID:960212; PIDN:CAA40693.1; PID:9388536
A:Experimental source: Strain JB8
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1991
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein

Query Match 93.5%; Score 43; DB 1; Length 219;
Best Local Similarity 90.0%; Pred. No. 0.13;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
:|||||||
Db 209 RPVSTQLL 218

RESULT 4

VCLJX
env polyprotein precursor - human immunodeficiency virus type 1 (strain KB-1-gp32)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp32
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 01-Mar-1996
C:Accession: B42995
R:Shimizu, H.; Hasebe, F.; Tsuchie, H.; Morikawa, S.; Ushijima, H.; Kitamura, T.
Virology 189, 534-546, 1992
A:Title: Analysis of a human immunodeficiency virus type 1 isolate carrying a truncated
A:Reference number: A42995; MUID:92315552; PMID:1322587
A:Accession: B42995
A:Molecule type: mRNA
A:Residues: 1-729 <SHI>
A:Cross-references: GB:S41266; GB:D01206
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-689/Domain: extracellular #status predicted <EXT>
F:1-33/Domain: signal sequence #status predicted <SIG>
F:17-33/Region: hydrophobic #status predicted
F:34-517/Product: coat protein gp120 #status predicted <CP1>
F:518-517/Region: cleavage processing #status predicted
F:518-729/Product: coat protein gp32 #status predicted <CP2>
F:518-514/Region: hydrophobic #status predicted
F:690-711/Domain: transmembrane #status predicted <TM1>
F:712-729/Domain: intracellular #status predicted <INT>
F:93,141,145,146,163,191,192,237,241,248,269,283,296,308,338,345,361,367,397,403,408,414

Query Match 93.5%; Score 43; DB 1; Length 729;
Best Local Similarity 90.0%; Pred. No. 0.51;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
:|||||||
Db 259 RPVSTQLL 268

RESULT 5

H44001

env polyprotein precursor - human immunodeficiency virus type 1 (strain YU-2)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Sep-1994
C:Accession: H44001
R:Li, Y.; Hui, H.; Burgess, C.J.; Price, R.W.; Sharp, P.M.; Hahn, B.H.; Shaw, G.M.
J Virol 66, 6587-6600, 1992
A:Title: Complete nucleotide sequence, genome organization, and biological properties of
A:Reference number: A44001; MUID:93021387; PMID:1404605
A:Accession: H44001
A:Molecule type: DNA
A:Residues: 1-843 <LTY>
A:Cross-references: GB:M93258
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: coat protein; glycoprotein; polyprotein; transmembrane protein
F:1-29/Domain: signal sequence #status predicted <SIG>
F:19-35/Region: hydrophobic
F:30-489/Product: coat protein gp120 #status predicted <GP1>
F:490-843/Product: coat protein gp41 #status predicted <GP2>
F:490-515/Region: hydrophobic
F:673-689/Region: hydrophobic
F:738-755/Domain: transmembrane #status predicted <TM1>
F:87,129,135,138,154,158,184,193,230,237,258,272,285,291,297,327,351,381,389,395,400,435

Query Match 93.5%; Score 43; DB 1; Length 843;
Best Local Similarity 90.0%; Pred. No. 0.6;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
:|||||||
Db 248 RPVSTQLL 257

RESULT 6

VCLJND
env polyprotein precursor - human immunodeficiency virus type 1 (isolate NDK)
N:Alternate names: coat polyprotein
N:Contains: coat protein gp120; coat protein gp41
C:Species: human immunodeficiency virus type 1, HIV-1
A>Note: host Homo sapiens (man)
C>Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 16-Jul-1999
C:Accession: J00066
R:Spire, B.; Sire, J.; Zachar, V.; Rey, F.; Barre-Sinoussi, F.; Galibert, F.; Hampe, A.;
Gene 81, 275-284, 1989
A:Title: Nucleotide sequence of HIV-1 NDK, a highly cytopathic strain of the human immunoc
A:Reference number: J00065; MUID:90034200; PMID:2806917
A:Accession: J00066
A:Molecule type: DNA
A:Residues: 1-846 <SPI>
A:Cross-references: GB:M27323; NID:9328154; PIDN:AAA44873.1; PID:9328162
A>Note: the authors translated the codon GCG for residue 523 as Arg
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyprot
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-501/Product: coat protein gp120 #status predicted <CP1>
F:502-846/Product: coat protein gp41 #status predicted <CP2>
F:502-520/Domain: transmembrane #status predicted <TM1>
F:674-692/Domain: transmembrane #status predicted <TM2>
F:87,129,151,179,182,229,236,257,271,284,290,351,382,388,392,395,401,438,451,452,601,606,

Query Match 93.5%; Score 43; DB 1; Length 846;
Best Local Similarity 90.0%; Pred. No. 0.6;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLL 10
:|||||||

Db 247 RPVSTQTL 256

RESULT 7

109448

envelope glycoprotein - human immunodeficiency virus type 1 (strain JRFL)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999

C:Accession: T09448

R:Panig, S.; Vintner, H.V.; Akeshi, T.; O'Brien, W.A.; Chen, I.S.; Koyanagi, Y.; Namazie,

submitted to the EMBL Data Library, July 1996

A:Reference number: Z16673

A:Accession: T09448

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-847 <PAM>

A:Cross-references: EMBL:U63632; NID:g1465777; PID:g1465781

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

Query Match 93.5%; Score 43; DB 2; Length 847;

Best Local Similarity 90.0%; Pred. No. 0.61;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSQTLL 10

Db 249 RPVSTQTL 258

RESULT 8

513289

env protein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997

C:Accession: S13289

R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.

Nature 348, 69-73, 1990

A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120

A:Reference number: S13288; PMID:91043044; PMID:2172833

A:Accession: S13289

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-847 <OBR>

C:Superfamily: type E retrovirus env polyprotein

Query Match 93.5%; Score 43; DB 2; Length 847;

Best Local Similarity 90.0%; Pred. No. 0.61;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSQTLL 10

Db 249 RPVSTQTL 258

RESULT 9

533985

env polyprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 26-Aug-1999

C:Accession: S33985

R:Carlini, F.

submitted to the EMBL Data Library, November 1991

A:Reference number: S33979

A:Accession: S33985

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-851 <CAR>

A:Cross-references: EMBL:Z15310; NID:g60192; PIDN:CAA7628.1; PID:g60199

C:Superfamily: type E retrovirus env polyprotein

Query Match 93.5%; Score 43; DB 2; Length 851;

Best Local Similarity 90.0%; Pred. No. 0.61;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSQTLL 10

Db 252 RPVSTQTL 261

RESULT 10

VCUJBR

env polyprotein - human immunodeficiency virus type 1 (isolate BR)

N:Alternate names: coat polyprotein

M:contains: coat protein gp120; coat protein gp41

C:Species: human immunodeficiency virus type 1, HIV-1

A:Note: host Homo sapiens (man)

C:Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Feb-1997

C:Accession: A31667

R:Rand, R.; Thayer, R.; Srinivasan, A.; Nayer, S.; Gardner, M.; Luciw, P.; Dandekar, S.

Virology 168, 79-89, 1989

A:Title: Biological and molecular characterization of human immunodeficiency virus (HIV-1)

A:Reference number: A94389; PMID:89085613; PMID:2789516

A:Accession: A31667

A:Molecule type: DNA

A:Residues: 1-852 <ANA>

C:Superfamily: type E retrovirus env polyprotein

C:Keywords: capsid protein; coat protein; polyprotein; transmembrane protein

F:1-516/Product: coat protein gp120 #status predicted <CP1>

F:517-852/Product: coat protein gp41 #status predicted <CP2>

Query Match 93.5%; Score 43; DB 1; Length 852;

Best Local Similarity 90.0%; Pred. No. 0.61;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSQTLL 10

Db 252 RPVSTQTL 261

RESULT 11

T12016

envelope glycoprotein - human immunodeficiency virus type 1 (strain sc14.3)

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000

C:Accession: T12016

R:McCutchan, F.E.; Sanders-Bell, E.; Salminen, M.O.; Carr, J.K.; Sheppard, W.H.

AIDS Res. Hum. Retroviruses 14, 329-337, 1998

A:Title: Diversity of the human immunodeficiency virus type 1 envelope glycoprotein in S

A:Reference number: Z17379; PMID:98178716; PMID:9519894

A:Accession: T12016

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-852 <MCC>

A:Cross-references: EMBL:U90934; NID:g2351783; PIDN:AAC59271.1; PID:g2351784

C:Genetics:

A:Gene: env

C:Superfamily: type E retrovirus env polyprotein

Query Match 93.5%; Score 43; DB 2; Length 852;

Best Local Similarity 90.0%; Pred. No. 0.61;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSQTLL 10

Db 251 RPVSTQTL 260

RESULT 12

S54384

envelope glycoprotein - human immunodeficiency virus type 1

C:Species: human immunodeficiency virus type 1, HIV-1

C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 26-Aug-1999

C:Accession: S54384

R:Theodore, T.; Buckler-White, A.J.

submitted to the EMBL Data Library, July 1989

A:Reference number: S54377
A:Accession: S54384
A:Status: preliminary
A:Molecule type: genomic RNA
A:Residues: 1-853 <TR>
A:Cross-references: EMBL:M2639; NID:G329377; PIDN:AAA45370.1; PID:G329385
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: polyprotein

Query Match 93.5%; Score 43; DB 2; Length 853;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLLL 10
:|||||||
Db 253 RPVSTQLLL 262

RESULT 13
S13288
env polyprotein - human immunodeficiency virus type 1
C:Species: human immunodeficiency virus type 1, HIV-1
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 31-Oct-1997
C:Accession: S13288
R:O'Brien, W.A.; Koyanagi, Y.; Namazie, A.; Zhao, J.Q.; Diagne, A.; Idler, K.; Zack, J.A.
Nature 348, 69-73, 1990
A:Title: HIV-1 tropism for mononuclear phagocytes can be determined by regions of gp120
A:Reference number: S13288; MUID:91043044; PMID:2172833
A:Accession: S13288
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-854 <OR>
C:Superfamily: type E retrovirus env polyprotein

Query Match 93.5%; Score 43; DB 2; Length 854;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLLL 10
:|||||||
Db 250 RPVSTQLLL 259

RESULT 14
VCLJZR
env polyprotein precursor - human immunodeficiency virus Zr-6
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus Zr-6
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 16-Jul-1999
C:Accession: D26192
R:Strinivasan, A.; Anand, R.; York, D.; Ranganathan, P.; Feorino, P.; Schochetman, G.; Cu
Gene 52, 71-82, 1987
A:Title: Molecular characterization of human immunodeficiency virus from Zaire: nucleot
A:Reference number: A26192; MUID:87248097; PMID:3036660
A:Accession: D26192
A:Molecule type: DNA
A:Residues: 1-855 <SR>
A:Cross-references: GB:K03458; GB:M16322; NID:G329398; PIDN:AAA45380.1; PID:G329403
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-19/Domain: signal sequence #status predicted <Sig>
F:20-85/Domain: signal sequence #status predicted <Sig>
F:20-85/Product: env polyprotein #status predicted <MAT>
F:20-500/Product: exterior membrane glycoprotein #status predicted <EXT>
F:501-855/Product: transmembrane glycoprotein #status predicted <TMM>
F:87,129,140,145,154,158,186,189,199,236,243,264,278,291,297,333,340,355,386,392,398,404

Query Match 93.5%; Score 43; DB 1; Length 855;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLLL 10

Db :|||||||
254 RPVSTQLLL 263

RESULT 15
VCLJH3
env polyprotein precursor - human immunodeficiency virus type 1 (isolate HTLV-III, BH10)
N:Alternate names: coat polyprotein
C:Species: human immunodeficiency virus type 1, HIV-1
A:Note: host Homo sapiens (man)
C:Date: 17-May-1985 #sequence_revision 17-May-1985 #text_change 16-Jul-1999
C:Accession: A03973
R:Ratner, L.; Haseltine, W.; Patarca, R.; Livak, K.J.; Starcich, B.; Joseph, S.F.; Dorar
nberger, U.A.; Papas, T.S.; Grzyb, J.; Chang, N.T.; Gallo, R.C.; Wong-Staal, F.
Nature 313, 277-284, 1985
A:Title: Complete nucleotide sequence of the AIDS virus, HTLV-III.
A:Reference number: A93353; MUID:85111123; PMID:2578615
A:Accession: A03973
A:Molecule type: DNA
A:Residues: 1-856 <RAT>
A:Cross-references: GB:M15654; GB:K02008; GB:K02009; GB:K02010; NID:G326383; PIDN:AAA4420
C:Genetics:
A:Gene: env
C:Superfamily: type E retrovirus env polyprotein
C:Keywords: AIDS; capsid protein; coat protein; glycoprotein; immunodeficiency; polyp
F:1-30/Domain: signal sequence #status predicted <Sig>
F:31-511/Product: exterior membrane glycoprotein #status predicted <TMM>
F:512-856/Product: transmembrane glycoprotein #status predicted <TMM>
F:88,136,141,156,160,167,197,230,234,241,262,276,289,295,301,332,339,356,386,392,397,406,
F:611,616,625,637,674,750,816/Binding site: carbohydrate (Asn) (covalent) #status predict

Query Match 93.5%; Score 43; DB 1; Length 856;
Best Local Similarity 90.0%; Pred. No. 0.61;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KPVSSTQLLL 10
:|||||||
Db 252 RPVSTQLLL 261

Search completed: March 12, 2004, 14:25:44
Job time : 22 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2004, 14:22:50 ; Search time 11 Seconds
(without alignments)
47.337 Million cell updates/sec

```
Title: PARKIN524.PEP
Perfect score: 46
Sequence: 1 kpvtstq111 10
```

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

```
Searched:      141681 segs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681
```

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	100.0	421	1	ENV_HV1S3	P12490 human immun
2	46	100.0	852	1	ENV_HV1S5	P19549 human immun
3	46	100.0	855	1	ENV_HV1OY	P20888 human immun
4	46	100.0	856	1	ENV_HV1IY	Q70626 human immun
5	46	100.0	859	1	ENV_HV1MA	P04583 human immun
6	100.0		867	1	ENV_HV1J3	P12489 human immun
7	43	93.5	460	1	ENV_HV1J3	P12491 human immun
8	43	93.5	843	1	ENV_HV1Y2	P35961 human immun
9	43	93.5	846	1	ENV_HV1ND	P18799 human immun
10	43	93.5	847	1	ENV_HV1S1	P19550 human immun
11	43	93.5	847	1	ENV_HV1W2	P05880 human immun
12	43	93.5	848	1	ENV_HV1YR	P20871 human immun
13	43	93.5	851	1	ENV_HV1B8	P04582 human immun
14	43	93.5	852	1	ENV_HV1B8	P12488 human immun
15	43	93.5	853	1	ENV_HV1EL	P04561 human immun
16	43	93.5	853	1	ENV_HV1ME	P19551 human immun
17	43	93.5	853	1	ENV_HV1Z2	P12487 human immun
18	43	93.5	855	1	ENV_HV1Z6	P04560 human immun
19	43	93.5	856	1	ENV_HV1S1	F03375 human immun
20	43	93.5	856	1	ENV_HV1H2	P04578 human immun
21	43	93.5	856	1	ENV_HV1H3	P04624 human immun
22	43	93.5	856	1	ENV_HV1AN	P05877 human immun
23	43	93.5	856	1	ENV_HV1EP	P03376 human immun
24	43	93.5	856	1	ENV_HV1W1	P18782 human immun
25	43	93.5	856	1	ENV_HV1Z8	P05881 human immun
26	43	93.5	861	1	ENV_HV1AR	P03377 human immun
27	43	93.5	861	1	ENV_HV1XB	P31819 human immun
28	43	93.5	863	1	ENV_HV1Z8	P05882 human immun
29	43	93.5	865	1	ENV_HV1H4	P04579 human immun
30	43	93.5	868	1	ENV_HV1C4	P05879 human immun
31	42	91.3	854	1	ENV_HV1A2	P03378 human immun
32	41	89.1	854	1	ENV_HV1C2	P17261 chimpanzee
33	38	82.6	856	1	ENV_HV1C3	P05878 human immun

34	34	73.9	224	1	DCU_LYCES	Q42463	lycoperisico
35	34	73.9	486	1	AS78 DROME	P09773	dirosophila
36	32	69.6	369	1	VY16 MYCEE	P47558	mycoplasma
37	32	69.6	638	1	VY32 CAEEL	Q20680	caenorhabditi
38	32	69.6	1317	1	RPOD_SYNY3	P73334	synchocystis
39	31.5	68.5	843	1	NUOG_STRO	Q9348	stretococcus
40	31.5	67.4	114	1	COJR_HUMAN	Q14548	homo sapien
41	31	67.4	264	1	VY36 SHEON	P46319	shewanella
42	31	67.4	417	1	YFM6 ECOLI	P46351	escherichia
43	31	67.4	459	1	TRME_BACSU	P45811	bacillus subtilis
44	31	67.4	484	1	PEN3_ADRE3	O8416	porcine adenovirus
45	31	67.4	531	1	UGRE_CAEEL	Q10941	caenorhabditis elegans

ALIGNMENTS

RESULT_1				
ID	ENV_HV1N5	STANDARD;	PRT;	421 AA.
AC	P12490:			
DT	01-OCT-1989 (Rel. 12, Created)			
DT	01-OCT-1989 (Rel. 12, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (New York-5 isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_TaxID=11698;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=66259728; Pubmed=3014529;			
RA	Wiley R.W., Rutledge R.A., Dias S., Folks T., Theodore T., Buckler C.E., Martin M.A.);			
RT	"Identification of conserved and divergent domains within the envelope gene of the acquired immunodeficiency syndrome retrovirus.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 83:5038-5042(1986).			
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CC	-----			
DR	EMBL; K03346; AAB02407.1; -.			
DR	HIV; K03346; ENV\$NYS.			
DR	InferPro; IPR000777; GP120.			
KM	Pfam; PF00516; GP120; 1.			
KM	AIDS; Coat protein; Polypotein; Glycopoltein; Transmembrane; signal.			
FT	SIGNAL.	1	30	
FT	CHAIN	31	421	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	DISUFLD	53	73	BY SIMILARITY.
FT	DISUFLD	118	200	BY SIMILARITY.
FT	DISUFLD	125	191	BY SIMILARITY.
FT	DISUFLD	130	152	BY SIMILARITY.
FT	DISUFLD	213	242	BY SIMILARITY.
FT	DISUFLD	223	234	BY SIMILARITY.
FT	DISUFLD	291	325	BY SIMILARITY.
FT	DISUFLD	378	410	BY SIMILARITY.
FT	CARBOHYD	87	87	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	97	97	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	129	129	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	135	135	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	140	140	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	151	151	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	155	155	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	183	183	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	192	192	N-LINKED (GLCNAC . .) (POTENTIAL).
FT	CARBOHYD	229	229	N-LINKED (GLCNAC . .) (POTENTIAL).

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FT CARBOHYD 236 236 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 257 257 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 271 271 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 284 284 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 326 326 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 349 349 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 395 395 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 421 AA; 47493 MW; 25A57519C22967B CRC64;

```

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Query Match 100.0%; Score 46; DB 1; Length 421;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KPVSSTOLL 10
Db 247 KPVSSTOLL 256

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RESULT 2
ENV_HV13 STANDARD; PRT; 852 AA.
ID ENV_HV13
AC P19549;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide Gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF33 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90317906; PubMed=2370688;
RA York-Higgins D., Cheng-Mayer C., Bauer D., Levy J.A., Dina D.;
RT "Human immunodeficiency virus type 1 cellular host range, replication, and cytopathicity are linked to the envelope region of the viral genome.";
RL J. Virol. 64:4016-4020 (1990).

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CC
CC EMBL, AY352275; AAQ17031.1;
CC PDB; IMBQ; 1I-DEC-02.
CC HIV; M38427; ENVSSR33.
CC InterPro; IPR000328; Env GP41.
CC InterPro; IPR000777; GP120.
CC Pfam; PF00515; GP120; 1.
CC DR AIDS; Coet protein; Polypeptide; Glycoprotein; Transmembrane; Signal;
CC 3D-structure.
CC SIGNAL 1 31
CC CHAIN 32 506 BY SIMILARITY,
CC CHAIN 507 852 EXTERIOR MEMBRANE GLYCOPROTEIN.
CC DISULFID 53 73 TRANSMEMBRANE GLYCOPROTEIN.
CC DISULFID 118 206 BY SIMILARITY.
CC DISULFID 125 197 BY SIMILARITY.
CC DISULFID 130 156 BY SIMILARITY.
CC DISULFID 219 248 BY SIMILARITY.
CC DISULFID 229 240 BY SIMILARITY.

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FT DISULFID 297 331 BY SIMILARITY.
FT DISULFID 377 439 BY SIMILARITY.
FT DISULFID 384 412 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 141 141 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 339 339 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 355 355 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 385 385 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 391 391 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 397 397 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 457 457 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 633 633 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 852 AA; 96663 MW; E87B8F8D23C991D0 CRC64;

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Query Match 100.0%; Score 46; DB 1; Length 852;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KPVSSTOLL 10
Db 253 KPVSSTOLL 262

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RESULT 3
ENV_HV10Y STANDARD; PRT; 855 AA.
ID ENV_HV10Y
AC P20888;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide Gp160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (OYI isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxID=11699;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90148544; PubMed=2559749;
RA Huet T., Dazza M.C., Brun-Vezinet F., Roelants G.B., Wain-Hobson S.;
RT "A highly defective HIV-1 strain isolated from a healthy Gabonese individual presenting an atypical western blot.";
RL AIDS 3:707-715(1989).

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CC -1- MISCELLANEOUS: THE OYI ISOLATE WAS TAKEN FROM THE BLOOD OF A
CC HEALTHY GABONESE INDIVIDUAL.
CC
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CC EMBL; M26727; AAA83397.1; -.
DR HIV; M26727; ENVSOY.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120.1.
DR Pfam; PF00517; GP41.1.
KW Aids; Coat protein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 509
FT CHAIN 510 855
FT DISULFID 53 73
FT DISULFID 118 210
FT DISULFID 125 201
FT DISULFID 130 162
FT DISULFID 223 252
FT DISULFID 223 244
FT DISULFID 301 335
FT DISULFID 381 442
FT DISULFID 388 442
FT DISULFID 87 87
FT CARBOHYD 134 134
FT CARBOHYD 142 142
FT CARBOHYD 145 145
FT CARBOHYD 161 161
FT CARBOHYD 165 165
FT CARBOHYD 192 192
FT CARBOHYD 202 202
FT CARBOHYD 239 239
FT CARBOHYD 246 246
FT CARBOHYD 267 267
FT CARBOHYD 281 281
FT CARBOHYD 284 284
FT CARBOHYD 300 300
FT CARBOHYD 306 306
FT CARBOHYD 336 336
FT CARBOHYD 359 359
FT CARBOHYD 389 389
FT CARBOHYD 395 395
FT CARBOHYD 399 399
FT CARBOHYD 405 405
FT CARBOHYD 458 458
FT CARBOHYD 610 610
FT CARBOHYD 615 615
FT CARBOHYD 624 624
FT CARBOHYD 636 636
FT CARBOHYD 815 815
SQ SEQUENCE 855 AA; 97476 MW; 9CF82A607AD62DA CRC64;

Query Match 100.0%; Score 46; DB 1; Length 855;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVVSTOLL 10
Db 257 KPVVSTOLL 266

RESULT 4
ENV_HV1LW STANDARD; PRT; 856 AA.
AC 070626;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV-1 isolate) (HIV-1).
OC Viruses; Retrovirdae; Retroviridae; Lentivirus.
OX NCBI_TaxId=82834;
RN [1]
```

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RP SEQUENCE FROM N.A.
RX MEDLINE=95127297; PubMed=7826699;
RA Reitz M.S. Jr., Hall L., Robert-Guroff M., Lautenberger J., Hahn B.M.,
RA Shaw G.M., Kong L.I., Weiss S.H., Waters D., Gallo R.C., Blattner W.;
RT "Viral variability and serum antibody response in a laboratory worker
RT infected with HIV type 1 (HIV type IIIB)."
RL Aids Res. Hum. Retroviruses 10:1143-1155(1994).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U12055; AAA76690.1; -.
DR PDB; 1IF3; 02-MAY-01.
DR GlycoSuiteDB; Q70626; -.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00517; GP41.1.
KW Aids; Coat protein; Glycoprotein; Glycoprotein; Transmembrane; Signal;
3D-structure.
FT SIGNAL 1 30
FT CHAIN 31 511
FT CHAIN 512 856
FT DISULFID 54 74
FT DISULFID 119 205
FT DISULFID 126 196
FT DISULFID 131 157
FT DISULFID 218 247
FT DISULFID 228 239
FT DISULFID 228 331
FT DISULFID 236 331
FT DISULFID 378 445
FT DISULFID 385 445
FT DISULFID 388 445
FT CARBOHYD 88 88
FT CARBOHYD 136 136
FT CARBOHYD 141 141
FT CARBOHYD 141 141
FT CARBOHYD 156 156
FT CARBOHYD 160 160
FT CARBOHYD 186 186
FT CARBOHYD 197 197
FT CARBOHYD 230 230
FT CARBOHYD 234 234
FT CARBOHYD 241 241
FT CARBOHYD 262 262
FT CARBOHYD 276 276
FT CARBOHYD 289 289
FT CARBOHYD 295 295
FT CARBOHYD 301 301
FT CARBOHYD 332 332
FT CARBOHYD 339 339
FT CARBOHYD 356 356
FT CARBOHYD 386 386
FT CARBOHYD 392 392
FT CARBOHYD 397 397
FT CARBOHYD 406 406
FT CARBOHYD 448 448
FT CARBOHYD 463 463
FT CARBOHYD 611 611
FT CARBOHYD 616 616
FT CARBOHYD 624 624
FT CARBOHYD 637 637
FT CARBOHYD 674 674
FT CARBOHYD 750 750
FT CARBOHYD 816 816
SQ SEQUENCE 856 AA; 96938 MW; 0C241332C7E56687 CRC64;

Query Match 100.0%; Score 46; DB 1; Length 856;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 159 159 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 199 199 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 246 246 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 253 253 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 307 307 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 366 366 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 402 402 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 408 408 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 412 412 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 418 418 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 460 460 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 475 475 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 636 636 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 648 648 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 867 AA; 98399 MW; 5F2310146B8E8680 CRC64;

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Query Match 100.0%; Score 46; DB 1; Length 867;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KPVSTOLL 10
Db 264 KPVSTOLL 273

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RESULT 7
ENV_HV123 STANDARD; PRT; 460 AA.
ID ENV_HV123
AC P1591;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor (Contains: Exterior membrane
glycoprotein (GP120)).
GN ENV.
OS Human immunodeficiency virus type 1 (Zaire 3 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11680;
RN [1]
RX MEDLINE=86259728; PubMed=3014529;
RA Buckley R.W., Rutledge R.A., Dias S., Folks T., Theodore T.,
Buckley C.E., Martin M.A.;
RT "Identification of conserved and divergent domains within the
envelope gene of the acquired immunodeficiency syndrome retrovirus";
RL Proc. Natl. Acad. Sci. U.S.A. 83:5038-5042(1986).
CC -1- MISCELLANEOUS. THOUGH THIS SEQUENCE CONTAINS A COMPLETE ENV CODING
REGION, INSERTION OF AN EXTRA NUCLEOTIDE CREATES A STOP CODON
PRIOR TO THE NORMAL TERMINATION; THE AUTHORS SUGGEST THAT THIS
VARIATION CAN ACCOUNT FOR THE LACK OF INECTIVITY OF THIS CLONE.
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CC -----
CC EMBL: K03347; AAA45372.1; -.
DR EMBL: K03347; AAA45373.1; -.
DR HIV: K03347; ENV523.
DR InterPro: IPR000777; GP120.
DR Pfam: PF00516; GP120.1.
KW Aids; Coat protein; Glycoprotein; Transmembrane;
Signal.
FT SIGNAL 1 29
FT CHAIN 30 460 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 202 BY SIMILARITY.
FT DISULFID 125 193 BY SIMILARITY.
FT DISULFID 130 149 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 225 236 BY SIMILARITY.
FT DISULFID 293 326 BY SIMILARITY.
FT DISULFID 372 439 BY SIMILARITY.
FT DISULFID 379 412 BY SIMILARITY.
FT DISULFID 397 404 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 292 292 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 460 AA; 51297 MW; 27B97EB75C7EFP50 CRC64;

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Query Match 93.5%; Score 43; DB 1; Length 460;
Best Local Similarity 90.0%; Pred. No. 0.24;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KPVSTOLL 10
Db 249 KPVSTOLL 258

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RESULT 8
ENV_HV1Y2 STANDARD; PRT; 843 AA.
ID ENV_HV1Y2
AC P35961;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor (Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)).
GN ENV.
OS Human immunodeficiency virus type 1 (YU-2 isolate) (HIV-1).
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=36377;
RN [1]
RX MEDLINE=93021387; PubMed=1404605;
RA Li Y., Hui H., Burgess C.J., Price R.W., Sharp P.M., Hahn B.H.,
Shaw G.M.;

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FT CARBOHYD 452 452 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 606 606 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 615 615 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 846 AA, 96476 MW, 8A3B9DA527DE2883 CRC64;

Query Match
Best Local Similarity 93.5%; Score 43; DB 1; Length 846;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSTOLL 10
Db 247 REVSTOLL 256

RESULT 10
ENV_HV1S1 STANDARD; PRT; 847 AA.
ID ENV_HV1S1
AC P19550;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (SF162 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentiviruses.
NCBI_Taxid=11691;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=90347835; PubMed=2384920;
RA Cheng-Mayer C., Quiroga M., Tung J.W., Dina D., Levy J.;
RT "Viral determinants of human immunodeficiency virus type 1 T-cell or macrophage tropism, cytopathogenicity, and CD4 antigen modulation.";
J. Virol. 64:4390-4398 (1990).
CC -----
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CC -----
CC EMBL: M65024; AAA5072.1; -
DR PDB: 10BE; 1S-MAT-97;
DR HIV; M38428; ENVSF162.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal; 3D-structure.
KW 3D-structure.
FT SIGNAL 1 29
FT CHAIN 30 502 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 503 847 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 73
FT DISULFID 118 BY SIMILARITY.
FT DISULFID 125 203 BY SIMILARITY.
FT DISULFID 130 194 BY SIMILARITY.
FT DISULFID 135 155 BY SIMILARITY.
FT DISULFID 154 144 BY SIMILARITY.
FT DISULFID 166 186 BY SIMILARITY.
FT CARBOHYD 195 195 BY SIMILARITY.
FT CARBOHYD 232 232 BY SIMILARITY.
FT CARBOHYD 239 239 BY SIMILARITY.

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FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 398 398 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 401 401 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 454 454 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA, 96135 MW, 0A901317FD7FE2AB CRC64;

Query Match
Best Local Similarity 93.5%; Score 43; DB 1; Length 847;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSTOLL 10
Db 250 REVSTOLL 259

RESULT 11
ENV_HV1W2 STANDARD; PRT; 847 AA.
ID ENV_HV1W2
AC P05880;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Envelope polypeptide GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (WMJ2 isolate) (HIV-1).
OC Viruses; Retroviridae; Lentiviruses.
NCBI_Taxid=11705;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=86235450; PubMed=3012778;
RA Hahn B.H., Shaw G.M., Taylor M.E., Redfield R.R., Markham P.D.,
RA Salathuddin S.Z., Wong S.T., Gallo R.C., Parks E.S., Parks W.P.;
RT "Genetic variation in HIV-1/II/LAV over time in patients with AIDS or at risk for AIDS.";
Science 232:1548-1553 (1986).
CC -!- MISCELLANEOUS: ISOLATES WMJ1, WMJ2, AND WMJ3 WERE OBTAINED FROM BLOOD SAMPLES SEQUENTIALLY TAKEN FROM A TWO-YEAR OLD HAITIAN WHO WAS PERINATALLY INFECTED BY HER MOTHER.
CC -----
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CC -----
CC EMBL: M12507; AAB12980.1; -
DR HIV; M12507; ENVSMW2.
DR InterPro; IPR000328; Env GP41.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane; Signal.
KW Signal.
FT SIGNAL 1 29
FT CHAIN 30 501 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 502 847 TRANSMEMBRANE GLYCOPROTEIN.

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FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 202 BY SIMILARITY.
FT DISULFID 125 193 BY SIMILARITY.
FT DISULFID 130 152 BY SIMILARITY.
FT DISULFID 215 244 BY SIMILARITY.
FT DISULFID 225 236 BY SIMILARITY.
FT DISULFID 229 326 BY SIMILARITY.
FT DISULFID 372 435 BY SIMILARITY.
FT DISULFID 379 408 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 140 140 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 155 155 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 184 194 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 259 259 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 273 273 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 327 327 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 334 334 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 356 356 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 380 380 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 386 386 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 438 438 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 450 450 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 602 602 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 616 616 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 628 628 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 847 AA; 96466 MW; CD1E3D73AABCAE CRC64;

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Query Match 93.5%; Score 43; DB 1; Length 847;
Best Local Similarity 90.0%; Pred. No. 0.43;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KPVVSTOLL 10
Db 249 RPVVSTOLL 258

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RESULT 12
ENV_HV1JR STANDARD; PRT; 848 AA.
AC P20871;
DT 01-FEB-1991 (Rel. 17, Created)
DT 10-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
OS ENV.
OC Human immunodeficiency virus type 1 (JRCSF isolate) (HIV-1).
OX NCBI_TaxID=11688;
RN [1]
RA Koyanagi S., Chen I.S.Y.;
RP Submitted (DEC-1988) to the HIV data bank.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).

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CC -----
DR EMBL; M38429; AAB03749.1; -.
DR PDB; 1GE4; 18-MAR-99.
DR HIV; M38429; ENVJRCSF.
DR InterPro; IPR000328; Env GP41.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR Pfam; PF00517; GP41; 1.
KW AIDS; Coat protein; Glycoprotein; Transmembrane; Signal;
KW 3D-structure.
FT SIGNAL 1 32
FT CHAIN 33 503
FT CHAIN 504 848
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 202 BY SIMILARITY.
FT DISULFID 125 194 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 216 245 BY SIMILARITY.
FT DISULFID 226 237 BY SIMILARITY.
FT DISULFID 294 328 BY SIMILARITY.
FT DISULFID 374 437 BY SIMILARITY.
FT CARBOHYD 381 410 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 239 239 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 260 260 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 274 274 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 299 299 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 329 329 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 382 382 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 388 388 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 392 392 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 403 403 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 440 440 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 453 453 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 603 603 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 617 617 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 808 808 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 848 AA; 96475 MW; 20767F51227ECF3 CRC64;

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Qy 1 KPVVSTOLL 10
Db 250 RPVVSTOLL 259

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Query Match 93.5%; Score 43; DB 1; Length 848;
Best Local Similarity 90.0%; Pred. No. 0.43;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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RESULT 13
ENV_HV1B8 STANDARD; PRT; 851 AA.
AC P04582;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
OS ENV.
OC Human immunodeficiency virus type 1 (BHR isolate) (HIV-1).
OX Viruses; Retroid viruses; Retroviridae; Lentivirus.

```

[illegible]

FT	CARBOHYD	811	811	N-LINKED (GLCNAC.) (POTENTIAL).
SO	SEQUENCE	851 AA;	96644 MW;	D16A3C90857785F1 CXC64;
Query Match		93.5%;	Score 43;	DB 1;
Best Local Similarity		90.0%;	Pred. No. 0.44;	
Matches	9;	Conservative	1;	Mismatches
			0;	Indels
			0;	Gaps
0y	1	KPVSTOLL	10	
	:			
Db	252	RPVSTOLL	261	
RESULT 14				
ENV_HV1EN				
ID	ENV_HV1BN	STANDARD;	PRT;	852 AA.
AC	P12488;			
DT	01-OCT-1989	(Rel. 12, Created)		
DT	01-OCT-1989	(Rel. 12, Last sequence update)		
DT	10-OCT-2003	(Rel. 42, Last annotation update)		
DE	Envelope polyprotein GP160 precursor [Contains: Exterior membrane glycoprotein (GP120); Transmembrane glycoprotein (GP41)].			
GN	ENV.			
OS	Human immunodeficiency virus type 1 (1BR isolate) (HIV-1).			
OC	Viruses; Retroid viruses; Retroviridae; Lentivirus.			
OX	NCBI_Taxid=11693;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89085613; PubMed=2789516;			
RA	Anand R., Thayer R., Srinivasan A., Nayyar S., Gardner M., Luciw P., Dandekar S.,			
RT	"Biological and molecular characterization of human immunodeficiency virus (HIV-1BR) from the brain of a patient with progressive dementia."			
RL	Virology 168:79-89 (1989).			
CC	-I- MISCELLANEOUS: THIS VIRUS IS CYTOPATHICALLY ACTIVE AND WAS HARVESTED FROM THE BRAIN TISSUE OF A NEUROLOGICAL AIDS PATIENT.			
CC	-----			
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CC	or send an email to license@1sb-sib.ch .			
CC	-----			
DR	EMBL; M21098; AAA44221.1; .			
DR	PIR; A31667; VCLJBR.			
DR	PDB; 1IM7; 23-OCT-02.			
DR	HIV; M21098; ENV\$BRVA.			
DR	InterPro; IPR000328; Env GP41.			
DR	InterPro; IPR000777; GP120.			
DR	Pfam; PF00516; GP120; 1.			
DR	Pfam; PF00517; GP41; 1.			
KW	AIDS; Coat protein; Polypotein; Glycoprotein; Transmembrane; Signal; 3D-structure.			
FT	SIGNAL	1	30	
FT	CHAIN	31	507	EXTERIOR MEMBRANE GLYCOPROTEIN.
FT	CHAIN	508	852	TRANSMEMBRANE GLYCOPROTEIN.
FT	DISULFID	54	74	BY SIMILARITY.
FT	DISULFID	119	205	BY SIMILARITY.
FT	DISULFID	126	196	BY SIMILARITY.
FT	DISULFID	131	155	BY SIMILARITY.
FT	DISULFID	218	247	BY SIMILARITY.
FT	DISULFID	228	239	BY SIMILARITY.
FT	DISULFID	296	330	BY SIMILARITY.
FT	DISULFID	376	439	BY SIMILARITY.
FT	DISULFID	383	412	BY SIMILARITY.
FT	CARBOHYD	49	49	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	88	88	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	135	135	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	138	138	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	154	154	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	158	158	N-LINKED (GLCNAC. .) (POTENTIAL).

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FT CARBOHYD 197 197 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 234 234 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 241 241 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 289 289 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 301 301 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 360 360 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 396 396 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 442 442 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 456 456 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 607 607 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 612 612 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 621 621 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 631 631 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 670 670 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 812 812 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 852 AA; 97203 MW; 2BB866345DEC915F CRC64;
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Query Match
Best Local Similarity 93.5%; Score 43; DB 1; Length 852;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 1 KPVVSTOLL 10
Db 252 RPVVSTOLL 261
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RESULT 15
ENV_HV1EL STANDARD; PRT; 853 AA.
AC P04581;
DT 13-AUG-1987 (Rel. 05, Last Created)
DT 13-AUG-1987 (Rel. 05, Last Sequence Update)
DT 16-OCT-2001 (Rel. 40, Last Annotation Update)
DE Envelope glycoprotein GP160 precursor [Contains: Exterior membrane
glycoprotein (GP120); Transmembrane glycoprotein (GP41)].
GN ENV.
OS Human immunodeficiency virus type 1 (HIV isolate) (HIV-1).
OC Viruses; Retroviridae; Retroviridae; Lentivirus.
OX NCBI_TaxID=11689;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=66245056; PubMed=2424612;
RA Alizon M., Main-Hobson S., Montagnier L., Sonigo P.;
RT "Genetic variability of the AIDS virus: nucleotide sequence analysis
of two isolates from African patients.";
RL Cell 46:63-74(1986).
```

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CC or send an email to license@isb-sib.ch).
```

```
CC -----
CC EMBL; K03454; AAA44329.1; -
CC DR EMBL; A07108; CAA00616.1; -
CC DR HIV; K03454; ENVSEI.
CC DR InterPro; IPR000328; ENV_GP41.
CC DR InterPro; IPR000777; GP120.
CC DR Pfam; PF00516; GP120; 1.
CC DR Pfam; PF00517; GP41; 1.
CC DR AIDS; Coat protein; Polypeptide; Glycoprotein; Transmembrane;
CC Signal.
CC FT SIGNAL 1 31 BY SIMILARITY.
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FT CHAIN 32 508 EXTERIOR MEMBRANE GLYCOPROTEIN.
FT CHAIN 509 853 TRANSMEMBRANE GLYCOPROTEIN.
FT DISULFID 53 73 BY SIMILARITY.
FT DISULFID 118 206 BY SIMILARITY.
FT DISULFID 125 197 BY SIMILARITY.
FT DISULFID 130 154 BY SIMILARITY.
FT DISULFID 219 248 BY SIMILARITY.
FT DISULFID 229 240 BY SIMILARITY.
FT DISULFID 297 330 BY SIMILARITY.
FT DISULFID 376 442 BY SIMILARITY.
FT DISULFID 383 416 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 129 129 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 235 235 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 242 242 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 263 263 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 277 277 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 290 290 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 353 353 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 384 384 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 394 394 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 405 405 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 406 406 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 411 411 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 445 445 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 458 458 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 459 459 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 462 462 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 608 608 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 613 613 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 622 622 N-LINKED (GLCNAC. . .) (POTENTIAL)
FT CARBOHYD 634 634 N-LINKED (GLCNAC. . .) (POTENTIAL)
SQ SEQUENCE 853 AA; 96721 MW; F9CD864DA0D07A5 CRC64;
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Query Match
Best Local Similarity 93.5%; Score 43; DB 1; Length 853;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
OY 1 KPVVSTOLL 10
Db 252 RPVVSTOLL 262
```

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Search completed: March 12, 2004, 14:24:18
Job time : 12 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2004, 14:22:50 ; Search time 40 Seconds
(without alignments)
78.880 Million cell updates/sec

Title: PARKIN524.PEP
Perfect score: 46
Sequence: 1 kpvstqlll 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL 25: *
1: sp_archaea: *
2: sp_bacteria: *
3: sp_fungi: *
4: sp_human: *
5: sp_invertebrate: *
6: sp_mammal: *
7: sp_mhc: *
8: sp_organelle: *
9: sp_phage: *
10: sp_plant: *
11: sp_rident: *
12: sp_virus: *
13: sp Vertebrate: *
14: sp_unclassified: *
15: sp_virus: *
16: sp_bacteriap: *
17: sp_archaeap: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	46	100.0	33	15	Q9QK19	Q9QK19 human immun
2	46	100.0	35	15	Q9J414	Q9J414 human immun
3	46	100.0	74	15	Q9J4H8	Q9J4H8 human immun
4	46	100.0	85	15	Q8J9C9	Q8J9C9 human immun
5	46	100.0	85	15	Q8J9C8	Q8J9C8 human immun
6	46	100.0	95	15	Q90U89	Q90U89 human immun
7	46	100.0	99	15	Q9Q767	Q9Q767 human immun
8	46	100.0	99	15	Q9Q780	Q9Q780 human immun
9	46	100.0	99	15	Q9J506	Q9J506 human immun
10	46	100.0	99	15	Q79317	Q79317 human immun
11	46	100.0	99	15	Q9Q779	Q9Q779 human immun
12	46	100.0	99	15	Q9J507	Q9J507 human immun
13	46	100.0	99	15	Q9J505	Q9J505 human immun
14	46	100.0	99	15	Q9J502	Q9J502 human immun
15	46	100.0	99	15	Q9Q778	Q9Q778 human immun
16	46	100.0	99	15	Q89210	Q89210 human immun

17	46	100.0	99	15	Q9Q769	Q9Q769 human immun
18	46	100.0	99	15	Q9Q771	Q9Q771 human immun
19	46	100.0	99	15	Q89206	Q89206 human immun
20	46	100.0	99	15	Q9Q773	Q9Q773 human immun
21	46	100.0	99	15	Q9Q770	Q9Q770 human immun
22	46	100.0	99	15	Q9J500	Q9J500 human immun
23	46	100.0	99	15	Q9Q772	Q9Q772 human immun
24	46	100.0	99	15	Q9J501	Q9J501 human immun
25	46	100.0	99	15	Q79318	Q79318 human immun
26	46	100.0	99	15	Q9Q775	Q9Q775 human immun
27	46	100.0	99	15	Q9J504	Q9J504 human immun
28	46	100.0	99	15	Q9J503	Q9J503 human immun
29	46	100.0	99	15	Q9Q774	Q9Q774 human immun
30	46	100.0	99	15	Q9Q768	Q9Q768 human immun
31	46	100.0	99	15	Q9Q777	Q9Q777 human immun
32	46	100.0	99	15	Q89196	Q89196 human immun
33	46	100.0	100	15	Q9YN56	Q9YN56 human immun
34	46	100.0	101	15	Q40202	Q40202 human immun
35	46	100.0	106	15	Q8JAS7	Q8JAS7 human immun
36	46	100.0	106	15	Q73212	Q73212 human immun
37	46	100.0	107	15	Q9YTT1	Q9YTT1 human immun
38	46	100.0	107	15	Q9WLD5	Q9WLD5 human immun
39	46	100.0	107	15	Q90580	Q90580 human immun
40	46	100.0	107	15	Q9YTS6	Q9YTS6 human immun
41	46	100.0	107	15	Q9YTS2	Q9YTS2 human immun
42	46	100.0	107	15	Q9WLD3	Q9WLD3 human immun
43	46	100.0	107	15	Q9YTS3	Q9YTS3 human immun
44	46	100.0	107	15	Q9YTS4	Q9YTS4 human immun
45	46	100.0	107	15	Q9YTS5	Q9YTS5 human immun

ALIGNMENTS

RESULT 1
ID Q9QK19 PRELIMINARY; PRT; 33 AA.

AC Q9QK19; 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2003 (TREMBlrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=220203.11;
RX MEDLINE=9909499; PubMed=9878014;
RA Van Dyke R.B., Korber B.T., Popok E., Macken C., Widmayer S.M.,
RA Bardeguet A., Hansen I.C., Wzina A., Luzuriaga K., Viscarello R.R.,
RA Wolinsky S., the Artel Core Investigators;
RT "The Artel Project: A prospective cohort study of maternal-child
RT transmission of human immunodeficiency virus type 1 in the era of
RT maternal antiretroviral therapy."
RL J. Infect. Dis. 179:319-326(1999).
DR EMBL; AF112548; AA13327.1; ..
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KW AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 33 AA; 3615 MW; 785F0B44BA535391 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 33;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVSSTOLL 10
|||||||

Db 13 KPVVSTQTL 22

RESULT 2

09J414 PRELIMINARY; PRT; 35 AA.
AC 09J414;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Truncated envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=TB24;
RA MEDLINE=20491829; PubMed=11035611;
RA Collins K.R., Mayanja-Kizza H., Sullivan B.A., Quinones-Mateu M.E.,
RA Toossi Z., Arts E.J.;
RT "Greater diversity of HIV-1 quasispecies in HIV-infected individuals
RT with active tuberculosis.";
RL J. Acquir. Immune Defic. Syndr. 24:408-417(2000).
DR EMBL; AF201787; AAF71854.1; -;
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein.
FT NON TER 1
SQ SEQUENCE 35 AA; 3497 MW; F424000992318A39 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 35;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVVSTQTL 10
Db 18 KPVVSTQTL 27

RESULT 3

09J4H8 PRELIMINARY; PRT; 74 AA.
AC 09J4H8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Truncated envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=TB24;
RA MEDLINE=20491829; PubMed=11035611;
RA Collins K.R., Mayanja-Kizza H., Sullivan B.A., Quinones-Mateu M.E.,
RA Toossi Z., Arts E.J.;
RT "Greater diversity of HIV-1 quasispecies in HIV-infected individuals
RT with active tuberculosis.";
RL J. Acquir. Immune Defic. Syndr. 24:408-417(2000).
DR EMBL; AF201793; AAF71860.1; -;
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Envelope protein; Glycoprotein.
FT NON TER 1
SQ SEQUENCE 74 AA; 8011 MW; 59A00D631924528A CRC64;

Query Match 100.0%; Score 46; DB 15; Length 74;
Best Local Similarity 100.0%; Pred. No. 0.037;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVVSTQTL 10
Db 18 KPVVSTQTL 27

RESULT 4

08J9C9 PRELIMINARY; PRT; 85 AA.
AC 08J9C9;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ARB169;
RA Ceballos A., Rabinovich R.D., Avila M.M., Martinez Peralta L.,
RA Gomez Carrillo M.;
RT "Molecular study of an HIV-1 transmission chain 7 years after
RT suspected events.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490622; AAM90890.1; -;
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
DR AIDS; Coat protein; Glycoprotein.
FT NON TER 1
SQ SEQUENCE 85 AA; 9372 MW; 70F92F1CB393D580 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KPVVSTQTL 10
Db 7 KPVVSTQTL 16

RESULT 5

08J9C8 PRELIMINARY; PRT; 85 AA.
AC 08J9C8;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retrovird viruses; Retroviridae; Lentivirus.
OX NCBI_Taxid=11676;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ARB168;
RA Ceballos A., Rabinovich R.D., Avila M.M., Martinez Peralta L.,
RA Gomez Carrillo M.;
RT "Molecular study of an HIV-1 transmission chain 7 years after
RT suspected events.";
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF490623; AAM90891.1; -;
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0019031; C:Viral envelope; IEA.

DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KM AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 85 AA; 9232 MW; 6034854CF928A3F5 CRC64;
Query Match 100.0%; Score 46; DB 15; Length 85;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVSSTOLL 10
DB 7 KPVSSTOLL 16
RESULT 6
Q90U89 PRELIMINARY; PRT; 95 AA.
AC Q90U89;
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21192328; PubMed=11294662;
RA Gunthard H.F., Havlir D.V., Fiscus S., Zhang Z.-Q., Bron J.,
RA Mollers J., Gulick R., Probst S.D., Leigh Brown A.J., Schleif W.,
RA Valentine F., Jones L., Melbohm A., Ignacio C.C., Isaacs R.,
RA Gamagami R., Smith E., Haase A., Richman D.D., Wong J.K.;
RT "Residual human immunodeficiency virus (HIV) type 1 RNA and DNA in
RT lymph nodes and HIV RNA in genital secretions and in cerebrospinal
RT fluid after suppression of viremia for 2 years.";
RL J. Infect. Dis. 183:1318-1327(2001).
DR EMBL; AF337312; AK56233.1; -;
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KM AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 95 AA; 10507 MW; DSA14913D1093609 CRC64;
Query Match 100.0%; Score 46; DB 15; Length 95;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVSSTOLL 10
DB 5 KPVSSTOLL 14
RESULT 7
Q90T67 PRELIMINARY; PRT; 99 AA.
AC Q90T67;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp120 C2V3 region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=subtype E;
RX MEDLINE=99408506; PubMed=10480629;
RA Kato K., Shino T., Kusagawa S., Sato H., Nohomi K., Shibamura K.,
RA Hien N.T., Chi P.K., Lien T.X., Anh M.H., Long H.T.,
RA Bunyarakvotin G., Fukushima Y., Honda M., Wasi C., Yamazaki S.,
RA Nagai Y., Takebe Y.;
RT "Genetic similarity of HIV Type 1 subtype E in a recent outbreak among
RT injecting drug users in Northern Vietnam to strains in Guangxi
RT province of Southern China.";
RL AIDS Res. Hum. Retroviruses 15:1157-1168(1999).
DR EMBL; AB025097; BA83669.1; -;
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KM AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 99 AA; 11109 MW; AAB1BA8E0DB38E13 CRC64;
Query Match 100.0%; Score 46; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVSSTOLL 10
DB 3 KPVSSTOLL 12
RESULT 8
Q90T80 PRELIMINARY; PRT; 99 AA.
AC Q90T80;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Envelope glycoprotein gp120 C2V3 region (Fragment).
GN ENV.
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
OX NCBI_TaxId=11676;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=subtype E;
RX MEDLINE=99408506; PubMed=10480629;
RA Kato K., Shino T., Kusagawa S., Sato H., Nohomi K., Shibamura K.,
RA Hien N.T., Chi P.K., Lien T.X., Anh M.H., Long H.T.,
RA Bunyarakvotin G., Fukushima Y., Honda M., Wasi C., Yamazaki S.,
RA Nagai Y., Takebe Y.;
RT "Genetic similarity of HIV Type 1 subtype E in a recent outbreak among
RT injecting drug users in Northern Vietnam to strains in Guangxi
RT province of Southern China.";
RL AIDS Res. Hum. Retroviruses 15:1157-1168(1999).
DR EMBL; AB025084; BA83656.1; -;
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0019031; C:viral envelope; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR000777; GP120.
DR Pfam; PF00516; GP120; 1.
KM AIDS; Coat protein; Glycoprotein.
FT NON_TER 1
SQ SEQUENCE 99 AA; 10954 MW; 504F1205EBF2D1C5 CRC64;
Query Match 100.0%; Score 46; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KPVSSTOLL 10
DB 3 KPVSSTOLL 12

RESULT 9

091506

ID 091506 PRELIMINARY; PRT; 99 AA.

AC 091506; 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

EN Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Subtype E;

RX MEDLINE=99146664; PubMed=10024059;

RA Kusagawa S., Sato H., Kato K., Nohomi K., Shino T., Samrith C.,

RT "HIV type 1 env subtype E in Cambodia."

RL AIDS Res. Hum. Retroviruses 15:91-94 (1999).

DR EMBL: AB013126; BAA3687.1; -

DR GO: GO:0019028; C:Viral capsid; IEA.

DR GO: GO:0019031; C:Viral envelope; IEA.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

KM AIDS; Coat protein; Glycoprotein.

FT NON_TER 1

SQ SEQUENCE 99 AA; 10927 MW; 773564329BF2D1DB CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLLL 10

Db 3 KPVVSTQLLL 12

RESULT 10

079317

ID 079317 PRELIMINARY; PRT; 99 AA.

AC 079317; 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

EN Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=JNH2T;

RX Takebe Y., Fujiwara Y., Sato H., Oka S., Pau C.P., Imai M., Ou C.Y.,

RT "Identification of Thai HIV-1 Variants in Japan (provisional title).";

RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.

DR EMBL: L32085; AAC37879.1; -

DR GO: GO:0019028; C:Viral capsid; IEA.

DR GO: GO:0019031; C:Viral envelope; IEA.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

KM AIDS; Coat protein; Glycoprotein.

FT NON_TER 1

SQ SEQUENCE 99 AA; 11012 MW; A07B123AE109DF23 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLLL 10

Db 3 KPVVSTQLLL 12

RESULT 11

090779

ID 090779 PRELIMINARY; PRT; 99 AA.

AC 090779; 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

EN Envelope glycoprotein gp120 C2V3 region (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Subtype E;

RX MEDLINE=99408506; PubMed=10480629;

RA Kato K., Shino T., Kusagawa S., Sato H., Nohomi K., Shbamura K.,

RT "HIV type 1 env subtype E in a recent outbreak among

RL injecting drug users in Northern Vietnam to strains in Guangxi

DR EMBL: AB025085; BAA3687.1; -

DR GO: GO:0019028; C:Viral capsid; IEA.

DR GO: GO:0019031; C:Viral envelope; IEA.

DR InterPro: IPR000777; GP120.

DR Pfam: PF00516; GP120; 1.

KM AIDS; Coat protein; Glycoprotein.

FT NON_TER 1

SQ SEQUENCE 99 AA; 10978 MW; B544B34E46A5A2C3 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVVSTQLLL 10

Db 3 KPVVSTQLLL 12

RESULT 12

091507

ID 091507 PRELIMINARY; PRT; 99 AA.

AC 091507; 01-NOV-1998 (TrEMBLrel. 08, Created)

DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

EN Envelope glycoprotein (Fragment).

GN ENV.

OS Human immunodeficiency virus 1.

OC Viruses; Retroid viruses; Retroviridae; Lentivirus.

OX NCBI_TaxID=11676;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Subtype E;

RX MEDLINE=99146664; PubMed=10024059;

RA Kusagawa S., Sato H., Kato K., Nohomi K., Shino T., Samrith C.,
 RA Leng H.B., Phalla T., Heng M.B., Takebe Y.,
 RT "HIV type 1 env subtype E in Cambodia."
 RL AIDS Res. Hum. Retroviruses 15:91-94(1999).
 DR EMBL: AB013127; BAA33686.1; -
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS: Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10966 MW; 92C67C25FE0731C0 CRC64;
 Query Match 100.0%; Score 46; DB 15; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSSTOLL 10
 Db 3 KPVSSTOLL 12

RESULT 13
 ID 091505 PRELIMINARY; PRT; 99 AA.
 AC 091505;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RX MEDLINE=99146664; PubMed=10024059;
 RC STRAIN=subtype E;
 RP SEQUENCE FROM N.A.
 RN (1)
 RA Kusagawa S., Sato H., Kato K., Nohomi K., Shino T., Samrith C.,
 RA Leng H.B., Phalla T., Heng M.B., Takebe Y.,
 RT "HIV type 1 env subtype E in Cambodia."
 RL AIDS Res. Hum. Retroviruses 15:91-94(1999).
 DR EMBL: AB013125; BAA33686.1; -
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS: Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 11007 MW; 3BD7758D878C2357 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSSTOLL 10
 Db 3 KPVSSTOLL 12

RESULT 14
 ID 091502 PRELIMINARY; PRT; 99 AA.
 AC 091502;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.

OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=subtype E;
 RX MEDLINE=99146664; PubMed=10024059;
 RA Kusagawa S., Sato H., Kato K., Nohomi K., Shino T., Samrith C.,
 RA Leng H.B., Phalla T., Heng M.B., Takebe Y.,
 RT "HIV type 1 env subtype E in Cambodia."
 RL AIDS Res. Hum. Retroviruses 15:91-94(1999).
 DR EMBL: AB013121; BAA33683.1; -
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS: Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10998 MW; 02DBE55EDA17FB85 CRC64;
 Query Match 100.0%; Score 46; DB 15; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSSTOLL 10
 Db 3 KPVSSTOLL 12

RESULT 15
 ID 090778 PRELIMINARY; PRT; 99 AA.
 AC 090778;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Envelope glycoprotein gp120 C2V3 region (Fragment).
 GN ENV.
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus.
 OC NCBI_Taxid=11676;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=subtype E;
 RX MEDLINE=99408506; PubMed=10480629;
 RA Kato K., Shino T., Kusagawa S., Sato H., Nohomi K., Shibamura K.,
 RA Hien N.T., Chi P.K., Lien T.X., Anh M.H., Long H.T.,
 RA Bunyaraksvotin G., Fukushima Y., Honda M., Wasi C., Yamazaki S.,
 RA Nagai Y., Takebe Y.,
 RT "Genetic similarity of HIV Type 1 subtype E in a recent outbreak among
 injecting drug users in Northern Vietnam to strains in Guangxi
 province of Southern China."
 RL AIDS Res. Hum. Retroviruses 15:1157-1168(1999).
 DR EMBL: AB025086; BAA83658.1; -
 DR GO: GO:0019028; C:Viral capsid; IEA.
 DR GO: GO:0019031; C:Viral envelope; IEA.
 DR GO: GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro: IPR000777; GP120.
 DR Pfam: PF00516; GP120; 1.
 KW AIDS: Coat protein; Glycoprotein.
 FT NON_TER 1
 FT NON_TER 99
 SQ SEQUENCE 99 AA; 10969 MW; 5050E7576E0731C5 CRC64;

Query Match 100.0%; Score 46; DB 15; Length 99;
 Best Local Similarity 100.0%; Pred. No. 0.05;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KPVSSTOLL 10
 Db 3 KPVSSTOLL 12

Search completed: March 12, 2004, 14:25:11
Job time : 42 secs
